OM protein

Run on:

Sequence:

```
neuroregenerative drug; glycogen synthase kinase-3; GSK-3; neurological disease; Parkinson's disease; Alzheimer's disease; Down's syndrome; cerebrovascular accident; stroke; spinal injury; Huntington's chorea; multiple sclerosis; amyotrophic lateral sclerosis; epilepsy; anxiety disorder; schizophrenia; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/partial
/product= "Human glycogen synthase kinase-3-related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "No stop codon is given"
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ADZ48946
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AEC31934
AEC81934
AEC81934
ADC99112
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ADC939
ACC78389
ACC78389
ACC78381
                            ADR40190
ADR5390
ADR5486
AAQ67459
ADD68695
AED6397
ABAC267
AD128892
AAQ67458
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                                                                                                                                                                                                                                                          ADR66574
ADR66232
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   Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-Q=Abs6/ABSWBBB spool/V310733816/runat_15092006_085442_15433/app_query.fasta_1
-Q=Abs6/ABSWBB spool/V310733816/runat_15092006_085442_15433/app_query.fasta_1
-DB=N Geneseq -QFWT=fastap -SUFFIX=p2n.zng -MINMÄTCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX-Eblosum62 -TRANS=human40.cdi -LiST=45
-DOCALIGN=200 -THR SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UOTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10733816_@CGN 1 1 2019 @runat 15092006_085442_15433 -NCPU=6 -ICPU=3
-NO NMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Aad11491 Human gly
Aca56816 Human sig
                                                                                                         September 17, 2006, 10:49:16; Search time 1231 Seconds (without alignments) 3347.359 Million cell updates/sec
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- 2006 Biocceleration Ltd.
                                                                            nucleic search, using frame_plus_p2n model
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , D
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Database

Result Š.

Total number Minimum DB 8 Maximum DB 6

Searched:

Adk11466 Human gly
Adi56612 Human pol
Adr40190 Human pol
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Adr40190 Human gly
Ada68695 Rat tau p
Ada68695 Rat tau p
Ada68695 Rat tau p
Ada68695 Rat tau p
Ada68698 Rat glyco
Adi2892 Mouse gly
Add686975 Human pro
Adr68745 Godes tau
Adf6869755 Human gly
Add69106 Human gly
Adv6922 Novel bro
Adr8946 Insulin s
Ade06992 Glycogen
Ade06999 Human GDN
Add1750 Human GDN
Add18030 Human GDN
Add18030 Human GJY
Adw1809 Human GJY

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TGGTCTGCTGCTGTGTTTGCTGAGCTGTTACTAGGACAACCAATATTTCCAGGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe
                                               TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg
                                                                  AspileLysProGlnAsnLeuLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp
                                                                                                                                GATATTAAACCGCAGAACCTCTTGTTGGATCCTGATACTGCTGTATTAAAACTCTGTGAC
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                                                                                                                                                                                                                                                                                                                                            The invention comprises a neuroregenerative drug that inhibits the activity of glycogen synthase kinase-3 (GSK-3). The neuroregenerative drug of the invention is useful for treating neurological disease, such as: Parkinson's disease, Alleimer's disease, Down's syndrome, cerebrovascular accident, stroke, spinal injury, Huntington's chorea, multiple sclerosis, amyotrophic lateral sclerosis, spilalipsyy, anxiety disorder, schizophrenia, depression and manic-depressive psychosis. The present human DNA sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                          940 TGGACTAAGGTCTTCCGACCCCGAACTCCACCGGAGGAATTGCACTGTGTAGCCCTCTG
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                               AGAGTTGCCAGACACTATAGTCGAGCCAAACAGACGCTCCCTGTGATTTATGTCAAGTTG
                                                                                 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg
                                                                                                    AspIleLysProGlnAsnLeuLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp
                                                                                                                                                                     580 GATAITAAACCGCAGAACCICTTGTTGGATCCTGATACTGCTGTATAAAACTCTGTGAC
                                                                                                                                                                                                                   PheGlySerAlaLygGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg
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               ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; probe; ss; array element; Parkinson's disease;
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                                                                                                                                                                                                                                                                                                                                                   The invention relates to antisense compounds targetted to nucleic acid encoding glycogen synthase kinase 3-beta (GSKB) (also known as tau protein kinase I (TPK-I)). The antisense compound is useful for inhibiting the expression of glycogen synthase kinase 3-beta enzyme the enzyme such as insulin regulation disorder, in particular diabetes and neurological disorder, e.g. Alzheimer's disease and bipolar illness. The antisense compound is also useful for diagnosing diseases associated with the expression of glycogen synthase kinase 3-beta and for whith the expression of glycogen synthase kinase 3-beta and for prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation and as a research reagent. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90
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                                                                                                                                                                                                                                                   Novel antisense compounds, particularly antisense oligonucleotides for inhibiting expression of glycogen synthase kinase 3 beta in cells and diagnosing, treating neurological and insulin regulation disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro
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                                  GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr
                                                          400 GAGAAGAAAGATGAGGTCTATCTTAATCTGGTGCTGGACTATGTTCCGGAAACAGTATACT
                                                                                                         151 ArgvalAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu
                                                                                                                                AGAGTTGCCAGACACTATAGTCGAGCCAAACAGACGCTCCCTGTGATTTATGTCAAGTTG
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                                                                                                                                                                                                    520 TATATGTATCAGCTGTTCCGAAGTTTAGCCTATATCCATTCCTTTGGAATCTGCCATCGG
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                                                                                                                                                                                                                                                                                580 GATATTAAACCGCAGAACCTCTTGTTGGATCCTGATACTGCTGTATTAAAACTCTGTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 SerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGln
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                                                                                                                                                                                                                                                                        polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an sequences mentioned in the specification. The combination is useful as an cray element in a microarray for monitoring the expression of a number of target polynucleotides. The microarray is particularly useful in the diagnosis and treatment of cancer and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, forensics and pharmacogenomics. The microarray is also useful for monitoring progression of diseases and for developing sophisticated combination is also useful for purifying a subpopulation of mRNAs, conditionance to endifferent signaling pathway populations which can be used to diagnose of and genomic fragments and in research and diagnostic applications. The various diseases including cancer e.g. adenocarcinoma and leukaemia, communopathies e.g. AIDS and astehma, neuropathies e.g. Alzheimer's disease and parkinson's disease. The present sequence represents a polynucleotide probable of the invention. Note: The sequence are for this patent did not form part of the printed specification but was obtained in electronic sequence in any answer and precipilation.
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                                                                                                                                                                                Combination of polynucleotide probes, useful as array elements in a microarray for monitoring the expression of a number of target
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Gaps:
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Best Local Similarity:
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The invention relates to novel Drosophila species DNA sequences and their encoded proteins with their corresponding human homologues. The proteins or their encoding polymuclectides are useful in a method of prevention, treatment or diagnosis of a disease in an individual, and used to identify a substance capable of binding to the polypeptide or modulating the polypeptide or modulating incubating the polypeptide. The compositions are administered to an individual in need of such treatment. The method of diagnosis, in which the presence or absence of a polymucleotide is detected in a biological sample, comprises brining the biological sample containing the nucleic acid such as DNA or concact with a probe comprising a fragment of at least 15 nucleotides of the polymucleotide, and detecting any duplex formed between the probe and nucleic acid in the sample. The method also comprises providing an antibody capable of binding to the polypeptide, incubating a biological sample with the antibody to allow the formation of an antibody-antigen complex, and determining whether antibody-antigen complex comprises such as cancer. The antibody to allow the formation of an antibody-antigen complex, and determining whether antibody-antigen complex compresses such as also useful in inhibiting the function. The diseases such as unclaimed a substance is also useful in inhibiting the function. The diseases such as substance is also useful in inhibiting the function. The diseases such as substance is also useful in inhibiting the function. The diseases such as substance is also useful in inhibiting the function. The diseases such as substance is also useful in inhibiting the function. The diseases such as substance is also useful in inhibiting the function. The diseases such as such as such as psoriasis, inflammatory diseases such as sequence represents a human homolog and an apportance of the processes of the inhibition of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Drosophila polypeptides and polynucleotides, useful for diagnosing, preventing and/or treating disorders, such as cancer, glomerulonephritis, rheumatoid arthritis, psoriasis, malaria, emphysema and alopecia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the Drosophila genes of the invention.
inflammatory disorder; malaria; emphysema; alopecia.
                                                                                                                                                                                                                                                                                                                                                                                                                      Glover D, Midgley C;
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27-NOV-2001; 2001GB-00028384.
11-FEB-2002; 2002GB-00003185.
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P-PSDB; ADK11467.
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                                                                                                      WO2003040301-A2
                                                       Homo sapiens
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Sequence 1389 BP; 402 A; 326 C; 326 G; 335 T; 0 U; 0 Other;

Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	1.55e-212 2024.00 100.0% 100.0% 97.3%	Length: Matches: Conservative: Mismatches: Indels:	1389 384 0 0 0	
orp. US-10-733-816-2 (1-394) x ADK11466 (1-1389)	x ADK11466 (daps: (1-1389)	o.	
11 MetSerGly	ArgProArgThrT	ChrThrSerPheAlaGluSerC	11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30	30
40 ATGTCAGG	CGGCCCAGAACCA	CCTCCTTTGCGGAGAGC	40 ATGTCAGGCCGGCCCAGAACCACCTCCTTTGCGGAGAGCTGCAAGCCGGTGCAGCAGCCT 99	66
31 SerAlaPhe	GlySerMetLysV	alSerArgAspLysAsp	31 SeralaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50	50
100 TCAGCTTT	GGCAGCATGAAAG	TTAGCAGAGACAAGGAC	TCAGCTTTTTGGCAGCATGAAGTTAGCAGAGACAAGGAGGCAAGGTGACAACAGTG 159	159

51	ValalathrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
71 220	ValilegiyasngiySerbhegiyValValValTyrginalaiysLeucysaspSergiygiu 90
91	LeuvalalaileiyskysvalLeudinaspiysargPheiysasnargduleudinile 110
111	MetargiysLeudaphisCysasnIleValargLeuargTyrPhePheTyrSerSerGly 130
131	GlulyslysaspgluvalTyrleuasnleuvalleuaspTyrvalprogluThrvalTyr 150
151	ArgvalalaargHisTyrSerargAlaLysGlnThrLeuProvalIleTyrValLysLeu 170
171	TyrwetTyrGlnLeuPheArgSerLeuAlaTyrlleHisSerPheGlylleCysHisArg 190
191	ASDII ELYSProGINASNieuleuleulaspProAspThrAlaValleulysleucyslasp 210
211	PheglySeralalysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
231	TYTTYTATGALABTOGIULEUILEPHEGIYALATHTASPTYTHTSETSETILEASDVAL 250
251	TrpSerAlaGlyCysValLeuAlaGluLeuLeuLeuGlyGlnProIlePheProGlyAsp 270
271	SerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGln 290
291	IleargGluMetAsnProAsnTyrThrGluPhelysPheProGlnIleLysAlaHisPro 310
311	TrpThrLysValBheArgProArgThrProProGlualalleAlaLeuCysSerArgLeu 330
331	LeuglutyrThrProThrAlaArgLeuThrProLeugluAlaCysAlaHisSerPhePhe 350
351	AspGluLeuArgAspProAsnValLySHiSProAsnGlyArgAspThrProAlaLeuPhe 370
371	AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390
391 1180	391 HisalaArgile 394

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The invention relates to a composition of polynucleotide probes

comprising first polynucleotide probes comprising at least a portion of a

gene encoding an effector-like polypeptide, second polynucleotide probes

comprising at least a portion of a gene encoding a transducing

polypeptide and third polynucleotide probes comprising at least a portion

composition are useful as array elements in a microarray for monitoring

the expression of target polynucleotides. The microarray for monitoring

the expression of target polynucleotides. The microarray is useful in the

diagnosis and treatment of cancer, an immunopathology or a

neuropathology. It can also be used for drug discovery and development,

toxicological and carcinogenicity studies, forensics or pharmacogenomics.

Microarrays can also be used for monitoring the progression of diseases

that may be associated with the altered expression of signalling pathway

polypeptides. The composition can also be used to purify a subpopulation

con manaba, or genomic fragments in a sample. The expression profile

is also useful for the diseases or depression. This sequence represents a

confinency Alzheimer's disease or depression. This sequence represents a

culcerative colities, or a neuropathology, e.g. dementia, ammesia,

confinency and not form part of the printed specification but was

confinency and one of the invention of the sequence data for

contained in electronic formet directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                               Human, probe, 88, receptor-like polypaptide; transducing polypeptide; effector-like polypeptide, cancer; immunopathology; neuropathology; drug development; toxicology; carcinogenicity; signalling pathway polypeptide; adrenal gland; bladder; bone; bone marrow; brain; breast; cervix; tumour; immunopathology; AlDS; diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology; dementia; amnesia; epilepsy; Alzheimer's disease; depression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New composition comprising polynucleotide probes, useful as array elements in a microarray for monitoring the expression of target polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
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                                                                                                                                                                                                                                                                                                               Human polynucleotide probe #1414.
                                                                               ADI56612 standard; DNA; 1389 BP.
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RESULT 5
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Length: Matches: Conservative: Mismatches:

1.55e-212 2024.00 100.0% 100.0%

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US-1	10-733-816·	-2 (1-394) x ADI	56612 (1-1	389)			
8 8	11	MetSerGlyArgPro	COARGIBATIBASE	erPheAlaGluS	rPheAlaGluSerCysLysProValC	1GlnGlnPro 3	0 0
3 8		5 5	Month control		or technology	The The Wal	
₹ 6	100	SerAtarneglyser TCAGCTTTTTGGCAGC	Metrysvals ATGAAAGTTP		Tarned-fyselmethyavalselmighabuyasabd-fyselmyava TTTTTTCACACATAAATTACAAAAAAAAAAAAAAAAAA	GACAACAGTG	
à			GlnGlyPro	spArgProglnG	luValSerTyrTh	rAspThrLys	0
qa	160	GTGGCAACTCCTGGG	CTGGGCAGGGTCCAG				19
ò	1.1	ValileGlyAsnGly	SerPheGlyV	AlvalTyrGlnA	GlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspS	erGlyGl	o
đ	220	GTGATT	TCATTTGGT	HILLILILI	CCAAACTTTGTGA	=ຽ	4
ò	91	LeuValAlaIleLys	LysValLeuG	llllllllll	AlailelysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnil	uleuGlnile 1	10
qq	280	CTGGT	AAAGTATTGC	AGGACAAGAGAT	TTAAGAATCGAGA		39
ò	111	MetarglysleudsphisCysdsnileValargleudrgTyrPhePheTyrS	HisCysAsn]	levalArgLeuA	rgTyrPhePheTy	rSerSerGly 1	3
qu	340		CACTGTAAC	ragrecearrec	<u> </u>	CCAGTGG	66
ò	131	GluLysLysAspGlu	ValTyrLeu	snLeuValLeuA	spTyrValProGl	uThrValTyr 1	20
q	400	GAGAAGAA	GTCTATCTTA	ATCTGGTGCTGG	ACTATGTTCCGGA	AACAGTATAC 4	59
ò	151	ArgvalAlaArgHis	TyrSerArg?	laLysGlnThrL	euProValileTy	rValLysLeu 1	20
셤	460	AGAGT	TATAGTCGAC	CCAAACAGACGC	CAGACACTATAGTCGAGCCAAACAGACGCTCCCTGTGATTTATGTCAAGTT	TGTCAAGTTG 5	19
ò	171	TyrMetTyrGlnLeu	PheArgSerI	euAlaTyrIleH	tTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisAr	eCysHisArg 1	
<u> </u>	520		Trecandr	TAGCCTATATCC	Arrecrirgaar	creccarces 5	62
ờ	191	AspileLysProGlnAsnLeuLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp	AsnLeuLeuI	JeuAspProAspT	hrAlaValLeuLy		210
셤	580		AACCTCTTG	regarcergara	CTGCTGTATTAAA	ACTCTGTGAC 6	e
ò	211	PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValS	GlnLeuValA	ArgGlyGluProA	snValSerTyrIleCysSe	eCysSerArg 2	
셤	640		cascresic	GAGGAGAACCCA	argiticgiatat	crerrcress 6	o
ò	231	TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal	GluLeuilei	PheGlyAlaThrA	SpTyrThrSerSe	rIleAspVal 2	2
셤	700		GAGTTGATCT	rtregaeccacre	Arrarccrcrag	raragargra 7	L)
ò	251	TrpSerAlaGlyCysValLeuAlaGluLeuLeuLeuGlyGlnProllePheP	ValLeuAlaC	3luLeuLeuLeuG	lyGlnProllePh	eProGlyAsp 2	120
g G	760		Grerrecer	agcretractae	GACAACCAATATT	rccagggar 8	_
ò	271	SerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGln	LeuValGlu]	[lelleLysValL	euGlyThrProTh	nrArgGluGln 2	06:
셤	820		TIGGTAGAA	ATAATCAAGGTCC	TGGGAACTCCAAC	PAGGGAGCAA 8	179
8	291	ΞΞ	ProAsnTyr	ThrGluPheLysP	eArgGluMetAsnProAsnTyrThrGluPhelysPheProGlnIleLysAlaHisPro		310
qq	880	Ā	CCAAACTAC	ACAGAATTTAAAT	тесетсаваттав	cacarccr	939
ð	311	TrpThrLysValPheArgProArgThrProFroGluAlaIleAlaLeuCysS	ArgProArg	ThrProProGluA	laileAlaLeuCy	erArgLeu	330
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ò	331		Thralaarg	LeuThrProLeuG	luAlaCysAlaHi		20
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disorder associated with erythroid cells e.g. anaemia and erythrocytosis, bone marrow e.g. leukaemia, platelets e.g. thrombocytopenia and thrombosis or Barcells and T-cells e.g. neutropenia. The compounds identified may be utilised during gene therapy procedures. The current sequence is that of a human haematological disorder-related cDNA of the
                                                                                                                                                                                                                                                                                       SerGlyvalAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGln
                                                                                                                                                                                                                                       ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys
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                                                                                                                                                                                                                                                    GTGGCAACTCCTGGGCAGGGTCCAGACAGCCCACAAGAAGTCAGCTATACAGACACTAAA
                                                                                                                                                                                                                                                                                                                                                                                         ValileGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                       CTGGTCGCCATCAAGAAAGTATTGCAGGACAAGAGATTTAAGAATCGAGAAGCTCCAGATC
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel method for identifying a compound capable of treating a haematological disorder which comprises combining a compound to be tested with a specific polypeptide under conditions suitable for binding of the test compound to the polypeptide. The method of the invention has haematological and cytostatic applications and may be useful for identifying compounds for treating a haematological
                                                                                                                                                                                                                                                                                        B-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a compound capable of treating a hematological disorder comprises combining a compound to be tested with a polypeptide related with the disorder under conditions suitable for binding of the test compound to the polypeptide.
     AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe
                   beta
                                                                                                                                                                                                                                                                          haematological; cytostatic; erythroid; anaemia; erythrocytosis;
bone marrow; leukaemia; platelet; thrombocytopenia; thrombosis;
T-cells; neutropenia; gene therapy; human; ss; gene;
glycogen synthase kinase a beta; GSK3beta.
                                                                                                                                                                                                                                                    glycogen synthase kinase 3 beta (GSK3beta) (1521) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Human glycogen synthase kinase (GSK3beta) (1521) protein"
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03-APR-2003; 2003US-0466320P.
28-APR-2003; 2003US-0465224P.
13-MAY-2003; 2003US-0465924P.
26-AUG-2003; 2003US-0465924P.
26-AUG-2003; 2003US-049106P.
15-SEP-2003; 2003US-050197P.
15-SEP-2003; 2003US-050199P.
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AGTGGTGTGGATCAGTTGGTAGAATAATCAAGGTCCTGGGAACTCCAACAAGGGAGCAA
                                                                       ATCAGAGAAATGAACCCAAACTACACAGAATTTAAATTCCCTCAAATTAAGGCACATCCT
                                                                                                                                                                                                                       GATGAATTACGGGACCCAAATGTCAAACATCCCAAATGGGCGAGACACCTGCACCTTC
                                                                                                                     TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu
                                                                                                                                                                                                LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe
                                       IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               toxic effect, gene expression profile, hepatotoxicity, toxicity marker, toxicity progression, drug screening; primary rat hepatocyte toxicity modelling; gene, ds.
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2002US-0371413P.
2002US-0373601P.
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12-APR-2002; 2
09-MAY-2002; 2
09-MAY-2002; 2
09-WAY-2002; 2
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28-JAN-2003;
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Elashoff M;
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Length:
Matches:
Conservative:
Mismatches:

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349 100 409 120 469

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The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
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(ISIS-) ISIS PHARM INC
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                     Bennett F
Mckay R,
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TATATCCATTCCTTTGGGATCTGCCATCGAGACATTAAACCACAGAACCTCTTGCTGGAT 709
                                                                                                                                                             TIGCTAGGACAACCAATATTICCTGGGGACAGTGGTGGAGTCAGTTGGTGGAAATAATA 949
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leukopenia; immunostimulant; hyperproliferation; cytostatic;
glycogen synthase kinase 3-beta; GSK3-beta; ds.
                              CCTGATACAGCTGTATTAAAACTCTGCGACTTTGGAAGTGCAAAGCAGCTGGTCCGAGGA
                                                                      GAGCCCAATGTTTCATATATCTGTTCTCGGTACTACAGGGCACCAGAGCTGATCTTTGGA
                                                                                                AlaThrAspTyrThrSerSerIleAspValTrpSerAlaGlyCysValLeuAlaGluLeu
                                                         GluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGly
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                    ProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antisense therapy; bone; bipolar disorder; neuroleptic; mania;
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                                                                                                                                                                                                                                                                                                                                                                                                    CCACCTCTGGCCACCATCCTTATCCCTCCTCACGCTCGGATT 1291
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04-DEC-2003; 2003US-0527397P.
04-DEC-2004; 2003US-0527420P.
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                                                                                                                                                                                                                                                                                        The invention comprises oligomeric compounds which are targeted to a nucleic acid molecule encoding a bone growth modulator chosen from dicktopf-1 (DKK-1), glycogen synthase kinase 3-beta, (GSK3-beta), sfrizzled-related protein 1 (SFRP-1), sclerostin, transducer of ERRB1, and src-c. The oligomeric compound of the invention is capable of inhibiting the expression of the bone growth modulator. The oligomeric compound of the invention is useful for inhibiting the expression of a bone growth modulator in a biological fluid, cell or tissue. The oligomeric compound of the invention is further useful in the treatment of bipolar disorder, mania, Alzheimer's disease, diabetes, leukopenia, sclerosteosis, and hyperproliferative disorders. The present nucleic acid represents a rat
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                                                                                                                    Novel oligomeric compound having nucleobases targeted to bone growth modulator nucleic acid, and inhibiting expression of bone growth modulator e.g., sclerostin, useful for inhibiting expression of bone
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  Jain
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Dobie KW,
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                                                                                                                                                                                                                                                 Example 2; SEQ ID NO 15; 357pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-733-816-2 (1-394) x AEA62866 (1-1525)
  Dean NM,
                         Myers K;
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2015.00
98.0%
98.0%
                                                                                                                                                                                                  growth modulator in animal.
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  Butler MM
                    Monia BP,
                                                                        WPI; 2005-435410/44
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Best Local Similarity:
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Pred. No.:
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us-10-733-816-2.p2n.rng

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AAQ67459 codes for a newly isolated tau-protein kinase I enzyme (TPK-1), shown in AAR61327 (compare to human AAR6136). The CDNA was cloned from a rat feeus brain cDNA library, and was expressed in insect cells. TPK-I acts specifically on tau-protein, which is thought to be involved in Alzheimer's disease (AD) and senile dementia of the AD type. It is hoped that the characterisation of TPK-I may lead to development of new agents for the prevention and therapy of these diseases. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)
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    with specificity for
treatment of Alzheimer'

                                                               Shiratsuchi
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                                                                Saito
                                                                                                                                        Newly isolated tau-protein kinase I enzyme protein providing means for prevention and disease.
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                        (MITU ) MITSUBISHI KASEI CORI
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                                                               Takashima A, Hoshino T,
                                                                                                    WPI; 1994-287181/36.
P-PSDB; AAR61327.
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                                                 TATATCCATTCCTTTGGGATCTGCCATCGAGACATTAAACCACAGAACCTCTTGCTGGAT
                                                                             ProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGly
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 CAGACACTCCCTGTGATCTATGTCAAGTTGTATATGTACCAGCTGTTCAGAAGTCTAGCC
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The invention relates to a novel method for the phosphorylation of tau protein in which tau protein or its partial peptide is phosphorylated by the action of phosphoenzyme I, a serine-threonine phosphorylase. The method of the invention may be used for elucidation of the cause of Alzheimer's disease and Alzheimer type senile dementia. The current sequence is that of the rat tau phosphorylation-related CDNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGCTGGACTATGTTCCGGAAACAGTGTACAGAGTCGCCAGACACTATAGTCGAGACAAG
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                                                                                                                                 CCTGATACAGCTGTATTAAAACTCTGCGACTTTGGAAGTGCAAAGCAGCTGGTCCGAGGA
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                                                                                                                                                                                                                                                                                AlaThrAspTyrThrSerSerIleAspValTrpSerAlaGlyCysValLeuAlaGluLeu
                                                                                                                                                                                                                                                                                                         GCCACCGATTACACGICTAGIATAGATGTATGGTCTGCAGGCTGTGTGTTGGCTGAATTG
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                                                                 TATATCCATTCCTTTGGGATCTGCCATCGAGACCATTAAACCACAGAACCTCTTGCTGGAT
                                                                                                                                                                                              GluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGly
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                                                                                                        ProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGly
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gene; serine-threonine phosphorylation.
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/*tag= a
/product= "Rat tau phosphorylation-related protein"
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                      rlleHisSerPheGlylleCysHisArgAsplleLysProGl
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The invention relates to a method of diagnosing (MI) a disease or disorder associated with aberrant glycogen synthase kinase-3beta (GSK-3beta) expression or activity, or a predisposition to the disease or disorder. by detecting marker within a GSK-3beta gene or its expression product that is associated with the disease or disorder in sample derived from a bubject, where detection is indicative of disease or disorder with the disease or disorder with the disease or disorder in a sample derived from a subject, where the categoric or disorder in a sample derived from a subject, where the categoric or disorder in a sample derived from a subject, where the categoric or disorder in the subject; identifying a marker within a GSK-3beta gene or disorder in the subject; identifying a marker within a GSK office or expression product that is associated with a marker is disorder that is associated with the marker; or determining a disease or disorder that is associated with the marker; or determining a disease or disorder that is associated with the marker; or determining a disease or disorder that is associated with the marker of single nuclectide polymorphism (SNP); chosen from a thymidine or cytosine at a position corresponding to nuclectide position or single nuclectide polymorphism (SNP); chosen from a thymidine at a position corresponding to nuclectide with aberrant glucose disorder, where the disease or disorder associated with aberrant glucose metabolism, stroke, stroke induced ischmia, muscle hypertrophy, cancer and their combinations. The disorder associated with aberrant glucose metabolism chosen from insulin resistance, type II aberrant glucose metabolism chosen from insulin resistance, type II disorder and their combinations. The disorder is a disorder represents the glycosen synthase kinase-3beta synthase combinations and their combinations of the present sequence represents the glycosen synthase kinase-3beta gSNL special control c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 TCAGCTTTTGGCAGCATGAAAGTTAGCAGAGACAAGGACGGCAGCAAGGTGACAACAGTG 352
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                                                                                                                                         Determining disease or disorder associated with aberrant glycogen synthase kinase-3 beta expression/activity or its predisposition, by detecting marker within kinase gene/its product that is associated with disease, in subject's sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 ATGTCAGGGCCCCAGAACCACCTCCTTTGCGGAGAGCTGCAAGCCGGTGCAGCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1600 BP; 485 A; 357 C; 362 G; 396 T; 0 U; 0 Other;
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Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                            6; SEQ ID NO 4; 308pp; English
(GARV-) GARVAN INST MEDICAL RES
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                                                                              WPI; 2005-779491/79.
P-PSDB; AEE06398.
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/*teg= a
/product= "Glycogen synthase kinase-3beta splice variant
(lacking exon 9)."
                                                                                                                                                              LeuLeuGlyGlnProllePheProGlyAspSerGlyValAspGlnLeuValGluIleIle
                                                                                                                                                                                                      Trecraegacaaccaararrrccreegeacagreereregaarcagreegagaaraara
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                         GAGCCCAATGTTTCATATATCTGTTCTCGGTACTACAGGGCACCAGAGCTGATCTTTGGA
                                                                                AlaThrAspTyrThrSerSerIleAspValTrpSerAlaGlyCysValLeuAlaGluLeu
                                                                                                                        GCCACCGATTACACGTCTAGTATAGATGTATGGTCTGCAGGCTGTGTGTTGGCTGAATTG
                                                                                                                                                                                                                                              LysvalleuGlyThrProThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGlu
                                                                                                                                                                                                                                                                                                                              PhelysPheProGlnIleLysAlaHisProTrpThrLysValPheArgProArgThrPro
    GluProAenValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycogen synthase kinase-3beta splice variant cDNA SEQ ID NO:4.
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09-NOV-2004; 2004US-0626455P.
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient
                             Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445 GTGGCAACTCCTGGGCAGGGTCCAGACAGGCCACAAGAAGTCAGCTATACAGACACTAAA
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16-MAR-2000; 2000US-0189862P.
25-MAY-2000; 2000US-0207454F.
9-UUN-2000; 2000US-0211314P.
18-UUL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-025581P.
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                                                                      GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr
                                                                                                          ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu
                                                                                                                                                        TATATGTATCAGCTGTTCCGAAGTTTAGCCTATATCCATTCCTTTGGAATCTGCCCATCGG
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antisense therapy; bone; bipolar disorder; neuroleptic; mania; antimanic; Alzheimera disease; neuroprotective; noctropic; diabetes; antidiabetic; leukopenia; immunostimulant; hyperproliferation; cytostatic; glycogen synthase kinas 3-beta; GSK3-beta; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention comprises oligomeric compounds which are targeted to a nucleic acid molecule encoding a bone growth modulator chosen from dickkopt. I (DKK.), glycogen synthase kinase 3-beta, (GSK3-beta), sfrizzled-related protein 1 (SFRP-1), sclerostin, transducer of BRRB1, and src.. The oligomeric compound of the invention is capable of inhibiting the expression of the bone growth modulator. The oligomeric compound of the invention is useful for inhibiting the expression of a bone growth modulator in a biological fluid, cell or tissue. The oligomeric compound of the invention is further useful in the treatment of bipolar disorder, mania, Alzheimer's disease, diabetes, leukopenia, sclerosteosis, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel oligomeric compound having nucleobases targeted to bone growth modulator nucleic acid, and inhibiting expression of bone growth modulator e.g., sclerostin, useful for inhibiting expression of bone growth modulator in animal.
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Matches:
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2003US-0527174P.
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2003US-0527370P.
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04-DEC-2003; 2
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04-DEC-2003; 2
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AsplysaspGlySerLysValThrThrValValAlaThrProGlyGlnGlyProAspArg

41

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glycogen synthase kinase 3-beta (GSK3-beta) DNA sequence - SEQ ID 17.

(first entry)

25-AUG-2005

Rat

BP.

DNA; 1474

standard;

AEA62868

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US-10-733-816-2 (1-394) x ADI28892 (1-1503)
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                                    TyrGlnAlaLysLeuCysAspSerGlyGluLeuValAlaIleLysLysValLeuGlnAsp 100
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             AAGCGATTTAAGAACCGAGAGCTCCAGATCATGAGAAAGCTAGATCACTGTAACATAGTC
                                                                                                                  ArgleuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu
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 ProGlnGluValSerTyrThrAspThrLysValIleGlyAsnGlySerPheGlyValVal
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The present sequence is that of cDNA encoding a constitutively active form of murine glycogen synthase kinase beta (GSK-1beta). GSK-1beta is a serine/threonine Kinase that may affect cellular processes including development, differentiation and proliferation. When dephosphorylated at Ser-9, the kinase activity of GSK-1beta is constitutively active. The invention relates to methods of altering cardiac-preferred expression in transgenic animals. An animal cell or animal is stably transformed with an expression cassettes comprising a cardiac-preferred promoter ADI28866 operably linked to a nucleotide sequence of interest, e.g. GSK-1beta. Expression cassettes, host cells and transgenic animals are provided. The transgenic animals may have an altered susceptibility to cardiopathology cardiopathology is especially a cardiomyopath such as familial hypertrophic cardiomyopathies, dilated cardiomyopathies, peripartum cardiomyopathy, restrictive cardiomyopathies, ischaemic heart disease, angina pectoris, myocardial infarction, hypertensive heart disease and endocarditis (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid molecule having inducible cardiac-preferred expression, useful for diagnosing or treating cardiac diseases, including ischemic heart disease, angina pectoris, myocardial infarction and
                                                                                                   transgenic;
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                                                 cardiovascular-gen.; cardiant; antianginal; gene therapy; myosin; enzyme; gene; ss.
Mouse glycogen synthase kinase 3-beta coding sequence
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Matches:
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Indels:
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                                                                                                                                                                                                                                               Location/Qualifiers
33. .1295
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P-PSDB; ADI28893.
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ADI28892 standard; cDNA; 1503 BP

ADI28892

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| MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGl

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AAQ67458 codes for a newly isolated tau-protein kinase I enzyme (TPK-1), shown in AAR61326 (compare to rat AAR61327). The CDNA was cloned from a rat fetus brain cDNA library, and was expressed in insect cells. TPK-I acts specifically on tau-protein, which is thought to be involved in Alzheimer's disease (AD) and senile dementia of the AD type. It is hoped that the characterisation of TPK-I may lead to development of new agents for the prevention and therapy of these diseases. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)
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    with specificity for tau-
treatment of Alzheimer's

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                                                                                                                                                                    Codes tau-protein kinase I (TPK-I), Alzheimer's disease.
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ing means for prevention and
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                                                          AAQ67458 standard; cDNA to mRNA; 2088
                                                                                                                                                                                                                                                           Location/Qualifiers
616. .1885
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93JP-00085143.
93JP-00191246.
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1173 CATGCTCGGATT 1184
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protein providing
disease.
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22-MAR-1993;
02-AUG-1993;
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21-APR-1995
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                                               GTGGCAACTCCTGGGCTCCAGACAGGCCACAAGAAGTCAGCTATACAGACACTAAA 795
576 TCAGCTTTTGGCAGCATGAAAGTTAGCAGAGACAAGGACGGCAGCAAGGTGACAACAGTG 735
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GENERAL INFORMATION:
APPLICANT: Madeline M. Butler
APPLICANT: Robert McKay
APPLICANT: Robert McKay
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 BETA EXPRES
TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 BETA EXPRES
CURRENT APPLICATION NUMBER: US/09/489,765A
CURRENT FILING DATE: 2000-01-19
NUMBER OF SEQ ID NOS: 85
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US-09-240-767-11493

US-09-949-016-4906

US-09-949-016-4906

US-09-949-016-181

US-09-949-016-181

US-09-941-1197-38

US-08-917-197-38

US-08-917-197-38

US-09-417-197-38

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                                                                                               September 17, 2006, 10:54:31
                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                   nucleic search, using
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                        Sequence 1114, Application US/09016434

Patent No. 6500938

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
ITILE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
ITILE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
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384
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRETY APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1414:
SEQUENCE CHARACTERISTICS:
LENGTH: 1389 base pairs
                                                                                                                                                                                                                                                          STREET: INCYTE PHARMACEUTICALS, STREET: 3174 PORTER DRIVE CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: USA
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APPLICATION NUMBER:
FILING DATE:
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity:
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IMMEDIATE SOURCE
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Pred. No.:
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DB:
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                                                                                                                                                      GTGGCAACTCCTGGGGCAGGGTCCAGAACAGAAGAAGTCAGCTATACAGACACTAAAA 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
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                               ATGTCAGGGCGCCCAGAACCACCTCCTTTGCGGAGAGCTGCAAGCCGGTGCAGCACCT 99
                                                                                                                                   ValalaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
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Sequence 2, Application US/08602264A

Patent No. 5837853

GENERAL INFORMATION:
TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
TITLE OF INVENTION: ARZHEIMER'S DISEASE,
TITLE OF INVENTION: Lau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)

NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ProGlnGluValSerTyrThrAspThrLysValIleGlyAsnGlySerPheGlyValVal 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 GCGGAGAGCTGCAAGCCAGTGCAGCAGCCTTCAGCTTTTGGTAGCATGAAAGTTAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 AlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLysValSerArg
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 144 mb.
COMPUTER: 18M Compatible
COMPUTER: 18M Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,264A
FILING DATE: February 20, 1996
                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEB: WENDEROTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., i
CITY: Washington
COUNTRY: D.C.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/204,091
FILING DATE: March 2, 1994
ATTORNEY/AGENT INFORMATION:
RAGISTRATION NUMBER: 33,367
REFERRINGE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA
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2015.00
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SEQUENCE CHARACTERISTICS:
LENGTH: 1972 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity:
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                       GTGATTGGAAATGGATCATTTGGTGTGTATATCAAGCCAAACTTTGTGATTCAGGAGAA 279
                                                                                                                                                   CTGGTCGCCATCAAGAAAGTATTGCAGGACAAGAGATTTAAAGAATCGAGAGCTCCAGATC 339
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                                                                ValileGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
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                       TATCAAGCCAAACTTTGTGACTCAGGAGAACTGGTGGCCATCAAGAAAGTTCTTCAGGAC
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Matches:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                               COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,018A
FILING DATE: Unne 5, 1995
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/204,091
FILING DATE: MARCH 2, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
                                                                                                                                                                                                                                                                                                                                                                     NAME: Warren M. Cheek, Jr.
REGISTRATION UNUBER: 33,367
REFRENCK, DOCKET UNBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEPAX:
                                                   CITY: Washington
COUNTRY: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 ir
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Best Local Similarity:
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Sequence 2, Application US/08461018A
Patent No. 6071694
GENERAL INFORMATION:
APPLICANT: AAKINIKO TAKASHIMA et al.
TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)

US-08-461-018A-2

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Matches:
Conservative:
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Indels:
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                                                                                         US/09/216,958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: cDNA to genomic RNA ORIGINAL SOURCE:
                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,018
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
            COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION WIMBER: US/09/2:
FILING DATE:
                                                                                                                                                                                                                            NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.82e-236
2015.00
98.0%
98.0%
96.8%
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1.44 mb
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Best Local Similarity:
Query Match:
DB:
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ArgleuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu 140
                                                                                                                                                GinThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla 180
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                                                                     ValLeuAspTyrValProGluThrValTyrArgValAlaArgHisTyrSerArgAlaLys
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                      GCCACCGATTACACGTCTAGTATAGATGTATGGTCTGCAGGCTGTGTGTTGGCTGAATTG
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Sequence 2, Application US/09216958
Patent No. 624859
GENERAL INFORMATION:
GENERAL INFORMATION:
ARTILE ARTHON: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
NUMBER OF SEQUENCES:
ADDRESSES: WENDERCOTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
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CITY: Washington
COUNTRY: D.C.
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382
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/204,091
FILING DATE: MARCh 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. CHeek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELEPHONICATION INFORMATION:
TELEPHONICATION INFORMATION:
                                                                                                                                                                                                                                                                  MOLECULE TYPE: cDNA to genomic RNA ORIGINAL SOURCE:
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2010.00
99.7%
99.5%
                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2088 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                 ORGANISM:
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INASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
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                                                                     TATATCCATTCCTTTGGGATCTGCCATCGAGACATTAAACCACAGAACCTCTTGCTGGAT
                                                                                                                                                                        GluProAsnValSerTyr11eCysSerArgTyrTyrArgAlaProGluLeuIlePheGly
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                                                  TyrlleHisSerPheGlylleCysHisArgAspIleLysProGlnAsnLeuLeuAsp
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                                                                                                                                                                                              GAGCCCAATGTTTCATATATCTGTTCTCGGTACTACAGGGCACCAGAGCTGATCTTTGGA
                                                                                                                                                                                                                                     AlaThrAspTyrThrSerSerIleAspValTrpSerAlaGlyCysValLeuAlaGluLeu
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                   CAGACACTCCCTGTGATCTATGTCAAGTTGTATATGTACCAGCTGTTCAGAAGTCTAGCC
                                                                                                             ProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGly
    CCACCTCTGGCCACCATCCTTATCCCTCCTCACGCTCGGATT 1291
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Patent No. 5837853
GENERAL INFORMATION:
TITLE OF INVENTION: PREVENTIVE OR THERAPEUTI
TITLE OF INVENTION: ARZHEMER'S DISRASE, A STITLE OF INVENTION: tau-PROTEIN KINASE I ORI NUMBER OF SEQUENCES: 14
CORRESPONDENCES: 14
CORRESPONDENCES: 18
ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700
CITY: Weahington
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIND & PONACK
Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 144 mb
COMPUTER: 18M Compartible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,264A
FILING DATE: February 20, 1996
CLASSIFICATION: 514
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US-08-602-264A-1
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382
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                              LENGTH: 2088 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to genomic RNA
ORIGINAL SOURCE:
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2010.00
99.7%
99.5%
96.6%
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INFORMATION FOR SEQ ID NO:
                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                   ORGANISM: human being
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Best Local Similarity:
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APPLICANT: Akihiko TAKASHIMA et al.
APPLICANT: Akihiko TAKASHIMA et al.
APPLICANT: Akihiko TAKASHIMA et al.
TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: ADDRESSE: ADDRESS:
COUNTRY: D.C.
ZIP: ADDRESSE: ADDRESS:
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Patent No. 6071694
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Matches:
Conservative:
Mismatches:
Indels:
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99.7%
99.5%
                human being
                                                                                                                   Percent Similarity:
Best Local Similarity:
 ORIGINAL SOURCE:
            , ORGANISM:
US-09-216-958-1
                                                                  Alignment Scores
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                                                                                                                                                                                            TGGACTAAGGTCTTCCGACCCCGGACTCCACCGGAGGCAATTGCACTGTGTAGCCGTCTG
                                SerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGln
                                                    AGTGGTGTGGATCAGTTGGTAGAAATAATCAAGGTCCTGGGAACTCCAACAAGGAGGAA
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Partent No. 6246559
GENERAL INFORMATION:
APPLICANT: ARABKINA:
APPLICANT: ARABKINA:
TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700
CITY: Weachington
COUWTRY: D.C.
ZIF: 20005
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,018
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA to genomic RNA
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MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 mb
COMPUTER: 1 EM COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/216,95
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TyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValPro
                                                                                                                   GluThrValTyrArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIle
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                                                                         APPLICANT: Robert McKay
APPLICANT: Madeline M. Butler
APPLICANT: Jacqueline Wyatt
TITLE OF INTO: ANTISENSE MODULATI
FILE REPERENCE: RTS-0115
CURRENT APPLICATION NUMBER: US/09/488,856A
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   AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe
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                                                                              CTGGAGTATACACCCAACTGCCCGGCTAACACCCACTGGAAGCTTGTGCACATTTTTT
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// OTHER INFORMATION: Incyte ID No. 6682888 234735.15
US-09-566-921-24
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Matches:
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                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Loring, Jeanne F.
APPLICANT: Infugley, Debora W.
TITLE OF INVENTION: GENES EXPRESSED IN ALZH
FILE REPRENENCE: PA-0024 US
CURRENT APPLICATION NUMBER: US/09/566,921
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                Sequence 24, Application US/09566921
Patent No. 6682888
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ORGANISM: Homo sapiens
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cal Similarity:
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Pred. No.:
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PERTURE:
NAME/KEY: MRNA
LOCATION: (1)...(1636)
OTHER INFORMATION: strain Columbia ecotype
OTHER INFORMATION: taxon:3702
OTHER INFORMATION: clone lib lambda ZaPII development stage young shoots
OTHER INFORMATION: Asson:3702
OTHER INFORMATION: Lissue type leaves
OTHER INFORMATION: Asson:3702
THERE INFORMATION: Clone lib lambda ZaPII development stage young shoots
PUBLICATION INFORMATION:
AUTHORS: Dornelas, M.C., Schwebel-Dugue, N., Thomas, M., Lecharny, A. and Kreis, M.
TITLE: Three New cDNAs Related to SGG/GSK-3 (Shaggy/Glycogen Synthase Kinase-3)
TITLE: from Arabidopsis thaliana (Accession No. 6822139 X94938, x94939 and X99595)
                                                                                                                                                          998 GTTTGGTCAGCTGGCTGTGTACTGGCAGAGCTCCTCTTGGGCCAGCCCATCTTCCCTGGG 1057
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AspPheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSer
                                                                  230 ArgTyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAsp
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Patent No. 6822139
GENERAL INFORMATION:
APPLICANT: Stawestdeutsche Saatzucht-SWS
APPLICANT: Advanta Seeds B.V.
TITLE OF INVENTION: Modulation of Storage Org.
FILE REFERENCE: 026-1
CURRENT APPLICATION NUMBER: US/09/578,194
CURRENT FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 1636
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JOURNAL: Plant Physiol
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ISSUE: 1
PAGES: 306-306
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Matches:
Conservative:
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                                                                     TYPE: DNA ORGANISM: Homo sapiens
CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
SEQ ID NO 3
LENGTH: 2154
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Percent Similarity:
Best Local Similarity:
                                                                                                                                         , LOCATION: (92)
US-09-488-856A-3
                                                                                                                         NAME/KEY: CDS
LOCATION: (92)
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                                           LysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeuLeuGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FALLEN, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinages
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/347,801
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,438
EARLIER FILING DATE: JUJ 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
SEQ ID NO 9
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Patent No. 6262345
GENERAL INFORMATION:
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ORGANISM: Zea mays
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Matches: 244
Conservative: 58
Mismatches: 70
Indels: 9
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DATE: 1997-01-01
DATABASE ACCESSION NUMBER: genbank/X94938
DATABASE ENTRY DATE: 1996-02-13
RELEVANT RESIDUES: (1)..(1636)
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        APPLICANT: Allen, Steve
APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TILLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: B8-1171
CURRENT APPLICATION NUMBER: US/09/854,731
CURRENT FILING DATE: 2001-05-14
FRIOR FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 9
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Fatent No. 6262345
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Plant Protein Kinases
FILE REPERENCE: BB-1171
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,438
EARLIER PILING DATE: J1999-07-07
SOFTWARE: MICROSOFT OF SEQ ID NOS: 23
SOFTWARE: MICROSOFT OF SEQ ID NOS: 23
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APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
TITLE REPERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/854,731
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 60/092,438
PRIOR FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
SEQ ID NO 15
LENGTH: 1673
                                                        Sequence 15, Application US/09854731 Patent No. 6794561 GENERAL INFORMATION:
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APPLICANT: Madeline M. Butler
APPLICANT: Madeline M. Butler
APPLICANT: Madeline M. Butler
APPLICANT: Madeline M. Butler
APPLICANT: Robert McKay
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 BETA EXPRESSION
TITLE OF INVENTION: ANTISENSE WOLLATION OF GLYCOGEN SYNTHASE KINASE 3 BETA EXPRESSION
CURRENT APPLICATION NUMBER: US/10/181,543
CURRENT FILING DATE: 2002-07-18
PRIOR PILING DATE: 2000-01-19
NUMBER OF SEQ ID NOS: 85
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1877, Apple Sequence 5, Appl Sequence 24, Appl Sequence 3, Appli Sequence 11, Appl Sequence 11, Appl Sequence 274, Appl Sequence 241, Appl Sequence 254, Appl Sequence 25972, Appli Sequence 2972, Appli Sequen
                                           Sequence 71, Appl
Sequence 256, App
Sequence 71, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 6, Appli
Sequence 6, Appli
                                                                                                                                                                                                                                             Sequence 30285, A
Sequence 17, Appl
Sequence 7, Appli
Sequence 1, Appli
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Sequence 21, Appl
Sequence 3081, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 49442, A
Sequence 9996, Ap
Sequence 30667, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 133605,
Sequence 23, Appl
Sequence 36269, A
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Sequence 32039,
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Sequence 61, A
Sequence 10, A
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US-11-136-527-2430

US-10-840-060-254

US-11-097-143-4571

US-10-292-408-2

US-10-437-963-29872

US-10-425-9-133605

US-10-292-408-2
                                                 US-10-62-674-1877
US-10-491-467-65
US-10-491-55-65
US-10-181-875-3
US-10-181-875-3
US-10-278-759-11
US-10-278-759-11
US-10-278-759-11
US-10-278-759-11
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US-10-770-726-21
US-11-136-527-3081
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Publication No. US20030211608A1
GENERAL INFORMATION:
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; LOCATION: (40)...(1302)
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1. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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                                                                                                                                                                                   September 18, 2006, 01:33:44; Search time 1472 Seconds (without alignments) 4933.419 Million cell updates/sec
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                               GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                     OM protein - nucleic search, using frame plus p2n model
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                            Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Match Length DB
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Jatabase :

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Result 80.

331 LeuGluTyrThrE 331 LeuGluTyrThrE 1000 CTGGAGTATACAC 351 AspGluLeuArgA 1060 GATGAATTACGG 371 AspPheThrThrC 1120 AcTTCACCCTT	Cy 391 High Land 118 394 Db 1180 CATCTCGCATT 1191 RESULT 2 US-10-305-720-1414 ; Sequence 1414, Application US/10305720 ; Publication No. US20040010136A1	; GENERALI INFORMATION: ; APPLICANT: AL-YOUNG, Janice K.; Seilhamer, Jeffrey J. ; TILLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression; ; TILLE REPERENCE: PA0002-1 CON ; FILE REPERENCE: PA0002-1 CON ; CURRENT APPLICATION NUMBER: US/10/305,720 ; CURRENT FILING DATE: 2002-11-26 ; PRIOR APPLICATION NUMBER: 09/016,434 ; RIOR APPLICATION NUMBER: 09/016,434 ; MUNDED OF SEC IN MOG. 1400		/ O'IBEX INFORMATION: Genbank ID NO. USZUG40ULUISOAL 9227230 US-10-305-720-1414 Alignment Scores: 1.16e-240 Length: 1389 Score: 2024.00 Matches: 384 Percent Similarity: 100.0\$ Conservative: 0 Best Local Similarity: 100.0\$ Mismacches: 0 Ouery Match: 77 Gaps: 0	US-10-733-816-2 (1-394) x US-10-305-720-1414 (1-1389) QY	Qy 31 SerAlaPheGlySerMetLy8ValSerArghspLy8AspGlySerLy8ValThrThrVal 50	Qy 71 ValileGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90 Db 220 GTGATTGGAAATGGATCATTTGGTGTGTGTGTATATCAAGCCAAACTTTGTGATTCAGGAGAA 279 Qy 91 LeuValAlalleLysValLeuGlnAsplySargPheLysAsnArGGluLeuGlnIle 110 Db 280 CTGGTCGCATCAAGAAAGTATTGCAGGACAAGAGATTTAAGAATCGAGAGCTCCAGATC 339 Qy 111 MeLArgLysLusabHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
Alignment Scores: 1.16e-240	31 SeralaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrThrVal 50	71 ValileGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90		151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProVallleTyrValLysLeu 170		231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250	271 SerGlyValAspGlnLeuValGluIleIleLvsValLeuGlyThrProThrArgGluGln 290

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         TITLE OF INVENTION: 5014

CURRENT APPLICATION NUMBER: US/10/772,636

CURRENT APPLICATION NUMBER: US/10/772,636

CURRENT FILING DATE: 2004-02-05

PRIOR PILING DATE: 2003-02-05

PRIOR PILING DATE: 2003-02-05

PRIOR PILING DATE: 2003-02-18

PRIOR PILING DATE: 2003-02-18

PRIOR PILING DATE: 2003-02-18

PRIOR PILING DATE: 2003-04-03

PRIOR PILING DATE: 2003-04-03

PRIOR PILING DATE: 2003-04-28

PRIOR PILING DATE: 2003-04-28

PRIOR PILING DATE: 2003-05-13

PRIOR PILING DATE: 2003-06-26

PRIOR PILING DATE: 2003-09-26

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PRIOR PILING DATE: 2003-09-15

PRIOR PILING DATE: 2003-09-15
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ORGANISM: Homo sapiens
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Publication No. US20050042687A1
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Carroll, Joseph M.
APPLICANT: Carroll, Joseph M.
APPLICANT: Farlow, Deborah
APPLICANT: Healy, Ailean
TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630, 71TLE OF INVENTION: 1472, 1762, 19290, 21690, 21699, 28899, 53659, 64549, 71TLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5891, 71TLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947, 71TLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
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ATGAGAAAGCTAGATCACTGTAACATAGTCCGATTGCGTTATTTTCTTCTACTCCAGTGGT 399
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PRIOR APPLICATION NUMBER: GB 0:
PRIOR FILING DATE: 2002-02-11
NUMBER OF SEQ ID NOS: 306
SOFTWARE: Patentin version 3.1
SEQ ID NO 256
LENGTH: 1389
                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
US-10-840-060-256
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publication No. US20050227243A1

GENERAL INPORMATION:
APPLICANT: Cyclacel Limited
APPLICANT: Deak, Peter
APPLICANT: Frenz, Lisa
APPLICANT: Midgley, Carol
TITLE OF INVENTYON: Cell Cycle Progression Proteins
FILE REFERENCE: 10069/2012
CURRENT FILING DATE: 2004-05-05
PRIOR APPLICATION NUMBER: US/10/840,060
CURRENT FILING DATE: 2004-05-05
PRIOR PLILING DATE: 2002-10-23
PRIOR PLILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: GB 0126506.5
PRIOR APPLICATION NUMBER: GB 0128384.5
PRIOR FILING DATE: 2001-11-27
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Matches:
Conservative:
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Indels:
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                     ... (1302)
                                                                                  Percent Similarity:
Best Local Similarity:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (40).
US-11-288-493-71
                                                    Alignment Scores
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                                                                                  TGGACTAAGGTCTTCCGACCCCGAACTCCACCGGAGGCAATTGCACTGTGTAGCCGTCTG
                                           ATCAGAGAAATGAACCCAAACTACACAGAATTTAAATTCCCTCAAATTAAGGCACATCCT
                                                                      TrpThrLysValPheArgProArgThrProProGluAlalleAlaLeuCysSerArgLeu
                                                                                                                LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe
                               IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 71
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                                                                                                                                                                                                                                                                                                            Sequence 71, Application US/11288493
Publication No. US20060078947A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                           HisAlaArgile 394
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US-11-288-493-71
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                                          LysArgPheLysAsnArgGluLeuGlnIleMetArgLysLeuAspHisCysAsnIleVal
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US-10-504-173-44
; Sequence 44, Application US/10504173
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                                                                              Sequence 2, Application US/09866712
Sequence 2, Application US/09866712
Patent No. US20020058637A1
GENERAL INFORMATION:
APPLICANT: Akihiko TAKASHIMA et al.
TITLE OF INVENTION: METHODS OF INHIBITING TAU-PROTEIN KINASE I ACTIVITY
INHIBITING NEURONAL CELL DEATH AND TREATING ALZHEIMER'S
KINASE I (AS AMENDED)
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FILING DATE: December 21, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REGISTRATION NUMBER: 2001-0488/LC/00177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)721-8200
ProProLeuAlaThr1leLeuIleProProHisAlaArg11e
                                                                                                                                                                                 NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION NUMBER: US/09/866,712
PILING DATE: 30-MBY-2001
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Matches:
Conservative:
Mismatches:
Indels:
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MOLECULE TYPE: cDNA to genomic RNA
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SEQUENCE CHARACTERISTICS:
LBNGTH: 1972 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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SEQUENCE DESCRIPTION: SEQ ID
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2015.00
98.0%
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Percent Similarity:
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Pred. No.:
                                                         RESULT 7
US-09-866-712-2
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                                                                                                         311 TrpThrLysValPheArgProArgThrProProGluAla1leAlaLeuCysSerArgLeu
                                                                                                                                                                                                                                                                                 937 TGGACTAAGGTCTTCCGACCCCGAACTCCACCGGAGCAATTGCACTGTAGCCGTCTG
                                      TrpSerhlaGlyCygValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp
                                                         757 TGGTCTGCCTGGCTGTGTTGTGTTGTTACTAGGACAACCAATATTTCCAGGGGAT
                                                                                                                                                                                 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro
                                                                                                                                                                                                     877 ATCAGAGAAATGAACCCAAACTACACAGAATTTAAATTCCCTCAAATTAAGGCACATCCT
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OTHER INFORMATION: Description of Artificial Sequence: Coding nucleur INFORMATION: acid sequence of the transgene used for the OTHER INFORMATION: production of GSK-3 beta transgenic non-human OTHER INFORMATION: animals
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| Sequence 6, Application US/10482524
| Sequence 6, Application US/10482524
| Publication No. US20040261137A1
| GENERAL INFORMATION:
| APPLICANT: Smithkline Beecham PLC
| TITLE OF INTENTION: Models for Metabolic Disorders
| TITLE OF INTENTION: Models for Metabolic Disorders
| FILE REFERENCE: PG4458
| CURRENT FILING DATE: 2003-12-22
| PRIOR APPLICATION NUMBER: GB 0115570.4
| PRIOR PILING DATE: 2001-06-26
| PRIOR PILING DATE: 2001-06-26
| NUMBER: OF SEQ ID NOS: 8
| SOUTWARR: Patentin Ver: 2.1
| SEQ ID NO 6
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
Publication No. US200502028A1
GENERAL INFORMATION:
APPLICANT. Axordia Limited
TITLE OF INVENTION:
PILE REPERENCE: P101863W0
CURRENT APPLICATION NUMBER: US/10/504,173
CURRENT APPLICATION NUMBER: 020359.5
PRIOR APPLICATION NUMBER: 020359.5
PRIOR FILING DATE: 2002-02-02
NUMBER OF SEQ ID NOS: 135
SEQ ID NO 44
LENGTH: 1231
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ORGANISM: Homo sapiens
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                                                                                                               Sequence 3, Application US/10482524
; Bublication No. US20040261137A1
; GENERAL INFORMATION:
; APPLICANT: Smithkline Beecham PLC
; APPLICANT: Holder, Julie C
; TITLE OF INVENTION: Models for Metabolic Disorders
; FILE REFERENCE: PG4452.524
; CURRENT APPLICATION NUMBER: US/10/482,524
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB 0115570.4
; PRIOR FILING DATE: 2001-06-26
; PRIOR FILING DATE: 2002-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFFWARE: PatentIN Ver. 2.1
; SEQ ID NO
; LEWICH: 1389
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Matches:
Conservative:
Mismatches:
Indels:
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                                                       1141 CATGCTCGGATT 1152
                                  391 HisAlaArgile
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US-10-482-524-3
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Best Local Similarity:
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Pred. No.:
                                                                                                         US-10-482-524-3
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Matches:
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 30285
LENGTH: 1815
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                 NAME/KEY: misc feature
LOCATION: 1, 1814, 1815
OTHER INFORMATION: n = A,T,C
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Pred. No.:
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Sequence 30285 Application US/10357930

Publication No. US20040259086A1

GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Schlegel. Robert
APPLICANT: Monahan, John
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERP
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERP
FILE PERERENCE: MILOGORG

CURRENT APPLICATION NUMBER: US/10/357,930

CURRENT PILING DATE: 2003-02-04

PRIOR FILING DATE: 2000-02-16

PRIOR APPLICATION NUMBER: 60/189,862

PRIOR APPLICATION NUMBER: 60/189,862

PRIOR APPLICATION NUMBER: 60/189,862

PRIOR PILING DATE: 2000-03-16

PRIOR APPLICATION NUMBER: 60/189,862

PRIOR PILING DATE: 2000-03-16

PRIOR PILING DATE: 2000-03-16

PRIOR PILING DATE: 2000-03-16

PRIOR APPLICATION NUMBER: 60/207,454

PRIOR PILING DATE: 2000-06-09

PRIOR APPLICATION NUMBER: 60/211,314

PRIOR PILING DATE: 2000-06-09

PRIOR APPLICATION NUMBER: 60/219,007

PRIOR APPLICATION NUMBER: 60/219,007
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RESULT 14
US-09-866-712-1
; Sequence 1, Application US/09866712
; Patent No. US20020058637A1
; GENERAL INFORMATION:
APPLICANT: Akihiko TAKASHIMA et al.
; TITLE OF INVENTION: METHODS OF INHIBITING TAU-PROTEIN KINASE I ACTIVITY
INTIBITING NEURONAL CELL DEATH AND TREATING ALZHEIMER'S DISF
KINASE I (AS AMENDED)
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    GAGAAGAAAGATGAGGTCTACCTTAACCTGGTGCTGGACTATGTTCCGGAGACAGTGTGTAC
                                                                                                 AGAGTCGCCAGACACTATAGTCGAGCCAAGACACTCCCTGTGTGTCTATGTCAAGTTG
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CORRESPONDENCE BADRESSE:
ADDRESSES: WENDEROTH, LIND & PONACK
STREET: 2033 K Street, N.W., #800
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STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
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; Sequence 7, Application US/10613728
; Publication No. US20040010813A1
; GENERAL INFORMATION:
   APPLICANT: Cincinnati Children's Hospital Medical Center
   APPLICANT: Cincinnati Children's Hospital Medical Center
   APPLICANT: Cincinnati Children's Hospital Medical Center
   APPLICANT: Chicinnati Children's Hospital Medical Center
   ITLE OF INVENTION: EXPRESSION SYSTEM FOR TRANSGENESIS
   FILE REPERENCE: CHANG CANGS;
   FILE REPERENCE: CHANG CANGS;
   CURRENT PILING DATE: 2003-07-03
   PRIOR APPLICATION NUMBER: 60/393,525
   NUMBER: OF SEQ ID NOS: 10
   SOFTWARE: FREUER OF MINDORS 10
   SOFTWARE: PREUER OF MINDORS 10
   SOFTWARE MINDORS 10

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Mismatches:
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99.5%
96.6%
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COTHER INFORMATION: GSK-CAUS-10-613-728-7
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Best Local Similarity:
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NAME/KEY: CDS
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Pred. No.:
Score:
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US-10-613-728-7
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Sequence 13, Application US/10278759
; Publication No. US20030114382A1
; GENERAL INFORMATION:
; APPLICANT: Walsh, Kenneth
; TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/278,759
; CURRENT FILING DATE: 2002-10-23
; FRIOR APPLICATION NUMBER: US 60/350160
; PRIOR PILING DATE: 2001-10-29
; PRIOR FILING DATE: 2001-11-3
; RIOR FILING DATE: 2001-11-3
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 13
; SEQ ID NO 13
; LENGTH: 1639
                                                                                                                                                                                                                                                                                                                                                                 1395
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171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg
                                          1096 TATATGTATCAGCTGTTCCGAAGTTTAGCCTATATCCATTCCTTTGGAATCTGCCATCGG
                                                                              191 AspIleLysProGlnAsnLeuLeuLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp
                                                                                                                                                               PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrlys 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         676 TCAGCTTTTGGCAGCATGAAAGTTAGCAGAGCACAAGACGACGAGCAGCAACAACAACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        616 ATGTCAGGGCCCCAGAACCACCTCCTTTGCGGAGAGCTGCAAGCCGGTGCAGCCGCT
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                                                                                           PRILICATION NUMBER: US/09/866,712
PILING DATE: 30-May-2001
CLASSIFICATION NUMBER: US/09/866,712
PRIOR APPLICATION NUMBER: 09/216,958
PILING DATE: December 21, 1998
ATTORNEY/AGENT INFORMATION:
NAMME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 2001-0488/LC/00177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2088
382
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: human being SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                               TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2088 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
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Pred. No.:
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US-10-733	-816-2 (1-394) x US-10-278-759-13 (1-1639)	} &
	11 MetSerGlyArgFroArgThrThrSerPheAlaGluSerCysIysProValGlnGlnPro 30	QQ QQ
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QD	353 GTGGCAACTCCTGGGCAGGGTCCAGACAGGCCACAAGAAGTCAGCTATACAGACACTAAA 412	
<u>ک</u> ۾	71 ValileGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90 	
à	91 LeuValAlaileLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnile 110	
Dp	473 CTGGTCGCCATCAAGAAAGTATTGCAGACAAGAGATTTAAGAATCGAGAGCTCCAGATC 532	
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qa	533 ATGAGAAAGCTAGATCACTGTAACATAGTCCGATTGCGTTATTTCTTCTACTCCAGTGGT 592	
ò	131 GlulysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150	
qq	593 GAGAAGAAGAAGAAGAACTAATCTGGTGCTGGACTATGTTCCGGAAACAGTATAC 652	
ठे र	151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProVallleTyrValLysLeu 170 62.	
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ò	191 AspileLysProGlnAsnLeuLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210	
QQ	773 GATATTAAACCGCAGAACCTCTTGTTGGATCCTGATACTGCTGTATTAAAACTCTGTGAC	
ò	PheGlySerAlaLygGlnLeuValArgGlyGluProAgnValSerTyrIleCygSerArg	
qq	TTTGGAAGTGCAAAGCAGCTGGTCCGAGGAGAACCCAATGTTTCGTATATCTGTTCTCGG	
දි සි	231 TyrTyrArghlaProGluLeuilePheGlyAlaThrApDTyrThrSerSerileApDVal 250 893 TACTATAGGGCACCAGAGTTGATCTTTGGGGCCACTGATTATACCTCTAGTATAGATGTA 952	
Š	251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuLeuGlyGlnProllePheProGlyAsp 270	
qq	953 IGGICTGCTGTGTGTGTGTGGCTGAGCTGTTACTAGGACAACCAATATTTCCAGGGGAT 1012	
ò	271 SerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGln 290	
Ωp	1013 AGIGGIGGGAICAGTIGGIAGAAAIAAICAAGGICCIGGGAACICCAACAAGGGAGCAA 1072	
ò	291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310	
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È	318 ArgThrProbroGluAlalleAlaLeucysSerArgLeuLeuGluTyrThrProThrAla 337 	

earch completed: September 18, 2006, 02:05:02 ob time : 1496 secs

84, Appl 56261, A 4, Appli

28735,

Sequence Sequence Sequence Sequence Sequence S 466629, 82942, A 23629, A 5, Appli 19717, A 46578, A

Sequence 13, Appl Sequence 262739, Sequence 223256, Sequence 115732, Sequence 217096, Sequence 285349, Sequence 316778, Sequence 26529, Sequence 26529, Sequence 19717, Sequence 19717, Sequence 19717, Sequence 117779, Sequence 13012, Sequence 33012, Sequence 23680, Sequence 31012, Sequence 21300, Sequence 21300,

19717, A 46578, A 33012, A 13202, A 4901, Ap 3109, A 5570, Ap

Sequence 1992, Ap Sequence 5085, Ap Sequence 43958, A

30399,

Sequence Sequence Sequence

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Sequence:

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Scoring table:

Searched:

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US-11-299-324-9

Sequence 9, Application US/11299324

Sequence 9, Application US/11299324

Publication No. US20060127388A1

GENERAL INFORMATION:

APPLICANT: Cain, Michael

APPLICANT: Tancor Novement of Glycogen Synthase Kinase 3 and Uses Thereof

TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof

FILE REFERENCE: WYE-052

CURRENT APPLICATION NUMBER: US/11/299,324

CURRENT APLICATION NUMBER: US 60/634,813

PRIOR FILING DATE: 2004-12-10

NUMBER OF SEQ ID NOS: 44

SEQ ID NO 9

LENGTH: 1263
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US-11-266-748A-56261
US-11-299-324-13
US-11-266-748A-262739
US-11-266-748A-273925
US-11-266-748A-323256
US-11-266-748A-323256
US-11-266-748A-15739
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US-10-449-902-19717
US-11-056-355B-46578
US-11-218-305-17779
US-11-056-35B-13202
US-11-056-355B-13202
US-11-056-355B-4901
US-10-449-902-24300
                  US-11-266-748A-381459
US-11-266-748A-381455
US-11-266-748A-28735
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US-11-266-748A-285349
US-11-266-748A-336778
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US-11-266-748A-466629
US-11-056-355B-82942
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US-11-056-355B-43958
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US-11-056-355B-12500
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Matches:
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-d-Abss/ABSGWEB spool/US10733816/runat_15092006_085458_15891/app_query.fasta_1
-DB=Published Applications NA New -OFMT=fastap -SIFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bIts -START=1 -END=-1 -MATRIX=blosum62
-LOOPCL=0 -LOOPEXT=0 -UNITS=bIts -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIGT=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-MAX.EN=2000000000 -HOST=abs805p
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-UND WMAP -NEG SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
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Sequence 3, Appli
Sequence 215, App
Sequence 1, Appli
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                                                                                                                                               September 18, 2006, 01:40:30 ; Search time 248 Seconds (without alignments) 4179.337 Million cell updates/sec
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11. FBM Celerra SIDS3/ptodata/1/pubpna/US09 NEW PUB.seq:*

22. FBMCCelerra SIDS3/ptodata/1/pubpna/US06_NEW-PUB.seq:*

23. FBMC Celerra SIDS3/ptodata/1/pubpna/US07 NEW PUB.seq:*

24. FBMC Celerra SIDS3/ptodata/1/pubpna/PCT NEW PUB.seq:*

25. FBMC Celerra SIDS3/ptodata/1/pubpna/DCT NEW PUB.seq:*

26. FBMC Celerra SIDS3/ptodata/1/pubpna/US10 NEW PUB.seq:*

27. FBMC Celerra SIDS3/ptodata/1/pubpna/US11 NEW PUB.seq:*

28. FBMC Celerra SIDS3/ptodata/1/pubpna/US11 NEW PUB.seq:*

39. FBMC Celerra SIDS3/ptodata/1/pubpna/US11 NEW PUB.seq:*

30. FBMC Celerra SIDS3/ptodata/1/pubpna/US11 NEW PUB.seq:*

30. FBMC Celerra SIDS3/ptodata/1/pubpna/US11 NEW PUB.seq:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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J Sequence 3, Application US/11299324

Publication No. US20060127388A1

Sequence 3, Application US/11299324

Publication No. US20060127388A1

APPLICANT: Cain, Michael

APPLICANT: Cain, Michael

APPLICANT: Cain, Michael

TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof

FILE REPERBNCE: WYE-052

CURRENT APPLICATION NUMBER: US/11/299,324

CURRENT FILING DATE: 2005-12-09

PRIOR APPLICATION NUMBER: US 60/634,813

PRIOR FILING DATE: 2004-12-10

NUMBER OF FILING DATE: 2004-12-10

NUMBER OF SEQ ID NOS: 44-12-10

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                 ATGTCAGGGGGGCCCAGAACCACCTCCTTTGCGGAGAGCTGCAAGCGGTGCAGCAGCCT
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rcent Similarity: 96.5\$ Conservativ st Local Similarity: 96.5\$ Mismatches: Ery Match: 8 Gaps:	US-10-/33-816-2 (1-394) X US-11-283-329-215 (1-1639) Qy	Db 233 AIGICAGGGGGCCAGAACCCCCCTTTGGGAGAGCTGCAAGCGGGGGGCAGCT 292 Qy 31 SeralaPheGlySerMetLysValSerArgAsplysAspGlySerLysValThrThrVal 50	Db 293 TCAGCTTTTGGCAGCATGAAAGTTAGCAGAGACAACGGCAGCAGCAGCAGCAGCAGCAGCAGCA	Db 353 GTGGCAACTCCTGGGCAGGGTCCAGACGCCCAAAGATCAGCTATACAGACATAAAA 412 Ov 71 VallleGlvanGlvSerPheGlvValValValTvrGlnAlaLvsLeuCvsAapSerGlvGlu 90	413 GTGATTGGAAATGGATCATTTGGTGGGTATATCAAGCCAAACTTTGTGATTCAGGAGAA 47	1 Delvalaratien/Suysvaldendinkspryskrigfrien/Sasikrigorinendinie in [] [] [] [] [] [] [] [] [] [] [] [] []	<pre>Qy 111 MeCArgLySLeuAspH1SCySASh11eVa.ArgLeuArgTyrPherheTyrSerSerGty 130 </pre>	Qy 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150	151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu	DD 653 AGAGTIGCCAGACACIAIAGICGAGCCAAACAGACGCICCCIGIGAIITAIGICAAGTIG 712 Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190	Db 713 TATATGTATCAGCTGTTCCGAAGTTTAGCCTATATCCATTCCTTGGAATCTGCCATGGG 772 Ov 191 AsplleLv8ProGlnAsnLeuLeuLeuAspProAspThrAlaValLeuLv8LeuCv8Asp 210]	Oy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230	Oy 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250 by as makenancaccaccaccaccaccaccaccaccaccaccaccacc	251 TrpSerAlaGlyCysValleuAlaGluLeuLeuLeuGlyGlnProllePheProGlyAsp [271 SerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGln	1013 A		Qy 311 TrpThrLys	318 ArgThrProProGlualaIleAlaLeuCysSerArgLeuLeuGluTyrThrProThrAla 337
191 AsplieLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp	UY ZII FNEGIYSETALALYSGINLENVALATGGIYGINFTOASNVALSETIYTIIECYSSETATG Z30	Oy 231 TyrTyrargalaProGluLeuilePheGlyalaThraspTyrThrSerSerileAspVal 250	Qy 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270 Db 721 TGGTCTGCTGTGTTGGCTGTGTTAGTTAGGACAATATTTCCAGGGGAT 780	Qy 271 SerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGln 290 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro	841 AICAGAGAAAIGAACCCAAACIACACAGAAIITAAAIITCCICAAAITAAGGCACAICCI 30 311 TrothelysValbheargpro 31	Db 901 TGGACTAAGGATTCGTCAGGAACAGGACATTTCACCTCAGGAGTGCGGGTTTTCGACCC 960 Qy 318 ArgThrProProGluAlaIleAlaLeuCy8SerArgLeuLeuGluTyrThrProThrAla 337	Db 961 CGAACTCCACCGGAGCAATTGCACTGTGTAGCCGTCTGCAGAGTATACACCAACTGCC 1020 338 Ard.euThrProLeuGlualaCvaalaHisSerPheBheAspGluLeuArdAspProAsn 357	1021 CGACTAACACCACTGGAAGCTTGTGCACATTCATTTTTGATGAATTACGGGACCCAAAT	dy 358 VallyshigFroAsnGlyArgAspThrProAlaLeuPheAsnPheThrThrGlnGlnLeu 377	Oy 378 SerSerAsnProProLeuAlaThrIleLeuIleProProHisAlaArgile 394		Sequence 215, Application US/11283329; Publication No. US20060134670A1; GENERAL INFORMATION:	; APPLICANT: Piu, Fabrice ; TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR ; TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS	CURRENT APPLICATION NUMBER: 105/11/283,329 CURRENT FILING DATE: 2005-11-18 FIRING APPLICATION NUMBER: 60/629,811 PRIOR PRILING DATE: 2004-11-19	; NUMBER OF SEQ ID NOS: 242 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SRO ID NO 215	LENGTH: 1639 TYPE: DNA	CACANISM: Homo sapiens FEATURE: NAME/KEY: CDS FORMITON: (151)	; LOCATION: (233)(1534) ; OTHER INFORMATION: GSK-3 US-11-283-329-215	Alignment Scores: 2.61e-213 Length: 1639 Pred. No.: 2.61e-213 Matches: 383 Score:

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RESULT 5
US-11-299-324-1

| US-11-299-324-1
| Sequence 1, Application US/11299324
| Publication No. US2066127388A1
| GENERAL INFORMATION:
| APPLICANT: Cain, Michael |
| APPLICANT: Yaworsky, Paul J |
| TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof PILE REFERENCE: WIS-052 |
| FILE REFERENCE: WIS-052 |
| FILE REPERENCE: WIS-052 |
| FILE REPERENCE: WIS-056-12-09 |
| PRIOR PLICATION NUMBER: US 60/634,813 |
| PRIOR FILING DATE: 2004-12-10 |
| NUMBER OF SEQ ID NOS: 44 |
| SOFTWARE: Patentin version 3.3 |
| LENGTH: 1388
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ArgvalAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
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                                                                   171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg
                                                                                                                                                                                                                                                                                                             661 TACTATAGGGCACCAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGTA
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                        481 TATATGTATCAGCTGTTCCGAAGTTTAGCCTATATCCATTCCTTTGGAATCTGCCATCGG
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## Sequence 2. Application US/11299324

## Publication No. US20060127388A1

## GENERAL INFORMATION:

## APPLICANT: Cain, Michael

## APPLICANT: Taworsky, Paul J

## APPLICANT: Taworsky, Paul J

## APPLICANT: Taworsky, Paul J

## APPLICANT: Wariants of Glycogen Synthase Kinase 3 and Uses Thereof

## TITLE OF INVENTY DATE: 2005-12-09

## PRIOR APPLICATION NUMBER: US/11/299,324

## CURRENT FILING DATE: 2005-12-09

## PRIOR FILING DATE: 2004-12-10

## NUMBER OF SEQ ID NOS: 44

## SEQ ID NO 2

## CANON 3.3

## CANON 2

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## CANON 3.3

## CANON 3.3
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                                       ArgieuThrProleuGluAlaCysAlaHisSerPhePheAspGluLeuArgAspProAsn
                                                                                                          VallysHisProAsnGlyArgAspThrProAlaLeuPheAsnPheThrThrGlnGluLeu
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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CORGANISM: Homo sapiens
US-11-299-324-2
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                     RESULT 4
US-11-299-324-2
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                                                                  1140 TTTTTGATGAATTACGGGACCCAAATGTCAAACTACCAAATGGGGGAGACACCTGCA
                                                                                                                                            .020 CATCCTTGGACTAAGGTCTTCCGACCCGGAACTCCACCGGAGGAATTGCACTGTGTAGC
                                        900 GGGGATAGTGGTGGATCAGTTGGTAGAAATAATCAAGGTCCTGGGAACTCCAACAAGG
                                                                                                                             309 HisProTrpThrLysValPheArgProArgThrProProGluAlalleAlaLeuCysSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/11299324
; bublication No. US20060127388A1
; CENERAL INFORMATION:
    APPLICANT: Cain, Michael
; APPLICANT: Yaworsky, Paul J
; TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and TITLE OF INVENTION: Variants of Glycogen Synthase 3 and TITLE OF INVENTION: Variants of Glycogen Synthase 3 and TITLE OF INVENTION NUMBER: US/11/299,324
; CURRENT FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 60/634,813
; PRIOR APPLICATION NUMBER: US 60/634,813
; SOFTWARE: PATENTIN VARIED NOS: 44
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CRGANISM: Homo sapiens
US-11-299-324-6
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Matches:
Conservative:
Mismatches:
Indels:
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; TYPE: DNA
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x US-11-299-324-4 (1-1167)
CURRENT FILING DATE: 2005-12-09
PRIOR APPLICATION NUMBER: US 60/634,813
PRIOR FILING DATE: 2004-12-10
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
TYPE: DNA
TYPE: DNA
ORGANISM: Homo sapiens
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Publication No. US20060127388A1

RENDICATE INFORMATION:

APPLICANT: Cain, Michael

APPLICANT: Yaworsky, Paul J

TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof

TITLE OF INVENTION UNMBER: US/11/299,324
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                                                                             291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
                                                                                                                                                                                -----AAGGTCTTCCGACCCCGAACTCCACCGGAGGAATTGCACTGTGTAGCCGTCTG 864
                                                                                                                                                                                                                                        331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
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APPLICANT: Johnston, Karl
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT PILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105492.2
PRIOR FILING DATE: 2004-11-03
PRIOR PRIOR DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PLING DATE: 2004-11-03
PRIOR PRILING DATE: 2004-11-03
PRIOR PRILING DATE: 2004-11-03
PRIOR PRILING DATE: 2004-11-03
PRIOR PRILING DATE: 2005-01-14
PRIOR FILING DATE: 2005-01-14
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483396
SOFTWARR: PAEDILIT Version 3.3
                                       781 AGTGGTGTGGTTGGTTGGTAGAATAATC-----
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Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
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NAME/KEY: misc_feature
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| LOCATION: (2092)...(2092)
| OTHER INFORMATION: n is a, c,
US-11-266-7488-347876
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OTHER INFORMATION: n is a,
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MAME/KEY: misc feature
LOCATION: (2002)..(2002)
OTHER INFORMATION: n is a
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LOCATION: (2022)..(2022)
OTHER INFORMATION: n is
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LOCATION: (2057)..(2057)
OTHER INFORMATION: n is
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LOCATION: (61)..(61)
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                    827 GTGTGTCACCGCGACATCAAGCCCCAGAACCTGCTGGTGGACCCTGACCATGCTGTCCTC 886
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GluThrvalTyrArgvalAlaArgHisTyrSerArgAlaLysGlnThrLeuProvalIle
                                                                            TyrVallysLeuTyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGly
                                                                                                                 767 TATGTCAAGGTGTACATGTACCAGCTCTTCCGCAGCTTGGCCTACATCCACTCCCAGGGC
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publication No. US20060134663A1

general information:
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Kari
ITLE OF INVENTION: Methods of Using the Same
ITLE OF INVENTION: Methods of Using the Same
CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SEQ ID NO 381459
LENGTH: 2134
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| OTHER INFORMATION: n is a, c,
US-11-266-748A-381459
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LOCATION: (2024)..(2024)
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LOCATION: (1812)..(1878)
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LOCATION: (2022)..(2022)
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LOCATION: (176)..(255)
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LOCATION: (2057)..(205
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APPLICANT: Harkin, Ball
APPLICANT: Johnston, Patrick
APPLICANT: Harkin, Ball
APPLICANT: Harkin, Patrick
APPLICANT: Johnston, Patrick
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REPERRORE : 5815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-01-14
PRIOR FILING DATE: 2005-01-14
PRIOR FILING DATE: 2005-07-18
                                                                                                                                                                             Sequence 431255, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
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LOCATION: (257)..(323)
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                                               27 ValGlnGlnProSerAlaPheGlySerMetLygValSerArgAspLysAgGlySerLyg
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                                                267 PheProGlyAspSerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrPro
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APPLICANT: Johnston, Patrick
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REPERRORS: 5815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-07-18
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Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
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LOCATION: (2086)..(2086)

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LOCATION: (2114)

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1118 CARATCCGAGAGATGAACCCCAACTACAGGAGTTCAAGTTCCCTCAGATTAAAGCTCAC
                                                                                                                                                 PheAspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeu
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APPLICANT: Bodian. Dale
APPLICANT: Bodian. Sherif
APPLICANT: Atmar. Chandrika
APPLICANT: Latario, Brian
APPLICANT: Quincavalla, Joseph
TITLE OF INVENTION: High throughput functional genomic
CURRENT PAPLICATION NUMBER: US/10/553,520
CURRENT FILING DATE: 2003-10-14
PRIOR PILING DATE: 2003-04-18
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 84
LENGTH: 2169
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                                         ProMetGluGlyGly---GlyMetSerGlyArgProArgThrThrSerPheAlaGluSer
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Wethods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION WUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
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PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-03-14
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; Publication No. US20660134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
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                         APPLICANT: HEBERLEIN, ULRIKE
APPLICANT: HEBERLEIN, ULRIKE
APPLICANT: WOLFE, FRED
TITLE OF INVENTION: THE ROLE OF GLYCOGEN SYNTHASE KINASE-3 AND 7
TITLE OF INVENTION: ETHANOL-INDUCED BEHAVIORS
FILE REFERENCE: 316T-002010US
CURRENT APPLICATION NUMBER: US/10/795,135
CURRENT FILING DATE: 2004-03-05
PRIOR APPLICATION NUMBER: US60/452,486
PRIOR APPLICATION NUMBER: US60/452,486
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.3
SEQ ID NO 4
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Publication No. US20060099599A1
GENERAL INFORMATION:
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                                            121 GIGGCAACTCCTGGGCAGGGTCCAGACAGGCCACAAGAAGTCAGCTATACAGACACATAAA
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| US-11-299-324-13 |
| US-11-299-324-13 |
| US-11-290-31-10 |
| Publication No. US200601273881
| GENERAL INFORMATION:
| APPLICANT: Cain, Michael |
| APPLICANT: Yaworsky, Paul J |
| TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof FILE REFERENCE: WYE-052 |
| TURRENT APPLICATION NUMBER: US/11/299,324 |
| CURRENT FILING DATE: 2005-12-09 |
| PRIOR PILING DATE: 2004-12-10 |
| NUMBER OF SEQ ID NOS: 44 |
| SOFTWARE PATENTING NOS: 44 |
| SOFTWARE PATENTING NOS: 44 |
| SEQ ID NO 13 |
| LENGTH: 837 |
| LENGTH: 837
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AUTHORS
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
           PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg
                                                                                    TyrTyrArgAlaProGluLeullePheGlyAlaThrAspTyrThrSerSerIleAspVal
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Patent: WO 03040301-A 256 15-WAY-2003;
Cyclacel Limited (GB)
Location/Qualifiers
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Sequence 256 from Patent W003040301.
AX777402
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11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30

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ProAenValLysHisProAenGlyArgAspThrProAlaLeuPhe 370 ABRPHGThrThrGluLeuSerSerSerABRProProLeuAlaThrIleLeuIleProPro 390 LeuValGluIleIleLysValLeuGlyThrProThrArgGluGln 290 ProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310 SLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle AACTGCCCGACTAACACCACTGGAAGCTTGTGTGTGTTTTTT //SerpheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu)HisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly TATAGTCGAGCCAAACAGACGCTCCCTGTGATTTATGTCAAGTTG WalleuAlaGluLeuLeuLeuGlyGlnProIlePheProGlyAgp CCAAACTACACAGAATTTAAATTCCCTCAAATTAAGGCACATCCT PTGAAAGTTAGCAGAGACAAGGACGGCAGCAAGGTGACAACATG GlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys MetLysValSerArgAspLysAspGlySerLysValThrThrVal <u>Ş</u>∙

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/db_xref="InterPro: IPR0109371"
/d
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Kobayashi, S., Ishiguro, K., Omori, A., Takamatsu, M., Arioka, M.,
Imahori, K. and Uchida, T.
A cdc2-related kinase PSSALRE/cdk5 is homologous with the 30 kDa
subunit of tau protein kinase II, a proline-directed protein kinase
sssociated with microtubule
PESS Lett. 335 (2), 171-175 (1993)
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TREQIREMPRYTERKEPQIRAHPWTKVFRPRTPPEALALCSRLLEYTPTARLTPLEA
CHSFPDELRDPNVKLPNGRDTPALFNFTTQELSSNPPLATILIPPHARIQAASPPA
NATAASDTNAGDRGGTNNAASASASNST"
  1120 AACTICACCACTCAAGAACTGTCAAGTAATCCACCTCTGGCTACCATCCTTATTCCTCCT 1179
                                                                                                                                                                                               ROD 18-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murcidea; Muridae; Murinae; Rattus.
1 (bases 1 to 1825)
Ishiguro, K., Shizatsuchi, A., Sato, S., Omori, A., Arioka, M.,
Kobayashi, S., Uchida, T. and Imahori, K.
Glycogen synthase kinase 3 beta is identical to tau protein kinase
I generating several epitopes of paired helical filaments
                                                                                                                                                                                                                                                                                                tau protein Kinase.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
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Conservative:
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/strain="Sprague-Dawley"
/db xref="taxon:10116"
/tisue_type="brain cortex"
/dev stage="adult"
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Pred. No.:
Score:
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                                                                                                                137 GAAGGAAAAGGTGATTCAAGAAGAGCCATCATGTCGGGGGGGCGACCGAGAACCACCTCCTTT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                   317 CCACAGGAAGTCAGTTATACAGACACGAAAGTGGATTGGAAATGGATCATTTGGTGTGATA
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                                                                                                                                                                                                                                                                                                                                                 257 GATAAAGATGGCAGCAAGGTAACCACAGTAGTGGCAACTCCTGGCCAGGGTCCTGACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrGlnAlaLysLeuCysAspSerGlyGluLeuValAlaIleLysLysValLeuGlnAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           377 TATCAAGCCAAACTTTGTGATTCTGGAGAACTGGTTGCCATCAAGAAAGTTCTACAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysArgPheLysAsnArgGluLeuGlnIleMetArgLysLeuAspHisCysAsnIleVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    497 CGACTGCGGTATTTCTTCTTCTACTCGAGTGGTGAGAAGAAGAAGAAGAGGTCTACCTTAACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 ValLeuAspTyrValProGluThrValTyrArgValAlaArgHisTyrSerArgAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               557 GTGCTGGACTATGTTCCGGAGACAGTGTACAGAGTCGCCAGACACTATAGTCGAGGCCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 AlaThrAspTyrThrSerSerIleAspValTrpSerAlaGlyCysValLeuAlaGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  857 GCCACTGATTACACGTCCAGTAIAGATGTAIGGTCTGCAGGCTGTGTGTTGGCTGAATTG
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                                                                                                                                                                                                                                                                                     AsplysAspGlySerLysValThrThrValValAlaThrProGlyGlnGlyProAspArg
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                                                           ---MetSerGlyArgProArgThrThrSerPhe
                                                                                                                                                                        21 AlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLysValSerArg
US-10-733-816-2 (1-394) x AF156099 (1-1535)
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QQDDRQPGSVGSYTDTKVIGNGS FGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMR
KLDHCNI VRLRYFFYSSGEKKDBVYLNLUDVPFTVYRVARHYSRAKQTLPVITVKL
YMYQLFRSLAYIHSFGTGTRDITKPQNLLLDPDTAVLKLCDFGSAKQLYRGEPNVSYIC
SRYYRAPELI FGATDYTSSIDVWSAGCVLAELLLGQPI FPGDSGVDQLVBIIKVLGTF
TRAQIREMNPNYTEFKFPQIKAHPWTKYRFRFTPPBEATALCSRLLEYTPTARLTFLEA
CAHSFPDELRDPNVKLDNGRTFFALFNFTTGELSSNPPLATILI PPFHARIGAAASPPA
NATAASDTNAGDRGQTNNAASASASNSI"
                                                                                                                                             AF156099 1535 bp mRNA linear ROD 24-FEB-2000 Mus musculus glycogen synthase kinase 3 beta mRNA, complete cds.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Salameh, W.A., Guo, T.B., Chan, K.C. and Mitchell, A.P.
Testicular expression and hormonal control of glycogen synthase
ProleuglualaCygalaHisSerPhePheAspGluLeuargaspProasnValLysHis
                                                                                                                   ProAsnGlyArgAspThrProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsn
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/protein_id="AAD39258.2"
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                                                                                                                                                                                                                                                                                        1291
                                                                                                                                                                                                                                ProProLeuAlaThrileLeuIleProProHisAlaArgile 394
                                                                                                                                                                                                                                                                 CACCTCTGGCCACCATCCTTATCCCTCCTCACGCTCGGATT
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/db xref="taxon:10090"
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/note="mGSK3beta"
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Length: Matches: Conservative: Mismatches: Indels: Gaps:

1.26e-183 2015.00 98.0% 98.0% 96.8%

Percent Similarity: Best Local Similarity: Query Match: DB:

Alignment Scores:

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Pred. No.:

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ProGlualalleAlaLeuCysSerArgLeuLeuGluTyrThrProThrAlaArgLeuThr

ProLeuGluhlaCysAlaHisSerPhePheAspGluLeuArgAspProAsnValLysHis 360

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Takashima,A., Hoshino,T., Imahori,K., Saito,K.-i., Shiratsuchi,A.
                                                                                                                                                                                                                                                                                                                LeuLeuGlyGlnProIlePheProGlyAspSerGlyValAspGlnLeuValGluIleIle
                                                                                                                                                                                                                                                                                                                                890 TIGCTAGGACAACCAATATTTCCTGGGGACAGTGGTGGATCAGTTGGTGGAAAAATA
                                                                                                                                                                                                                                                                                                                                                                                       361 ProAsnGlyArgAspThrProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsn
GTGCTGGACTATGTTCCGGAAACAGTGTACAGAGTCGCCAGACACTATAGTCGAGCCAAG
                                                                                  TyrileHisSerPheGlyileCysHisArgAspileLysProGlnAsnLeuLeuLeuAsp
                                                                                                  710 CCTGATACAGCTGTATTAAAACTCTGCGACTTTGGAAGTGCAAAGCAGCTGGTCCGAGGA
                                                                                                                                                                                                GluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGly
                                                                                                                                                                                                             241 AlaThrAspTyrThrSerSerIleAspValTrpSerAlaGlyCysValLeuAlaGluLeu
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                                            ProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGly
                          GlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla
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Sequence 2 from patent US 6071694.
AR097211 GI:12805941
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	RESULT 9 BD181611 LOCUS BD181611 BD181611 ACCESSION Method of the phosphorylation of tau protein. ACCESSION Method of the phosphorylation of tau protein. ACCESSION BD181611.1 GI:30792529 KEYWORDS SOURCE RATTUS SP. CNGANISM Rat	JOURNAL Patent: JP 2002335983-A 1 26-NOV-2002; MITSUBISHI CHEMICAL CORP COMMENT OS Rattus 8P. (Fat) PN JP 2002335983-A/1 PD 26-NOV-2002 PF 30-ARF-2002 JP 2002129146 PI KOICHI ISHIGURO, SHOBU SATO, YO UCHIDA, KAZUTOMO IMAHORI PC C12N15/09,C12P21/02/C12N9/12,C12N15/00 CC Strandedness: Double; CC Topology: Linear; CC Topology: Linear; FH Key FT source 1. 1932	FEATURES FT Location/Qualifiers source 1.1972 I.1972 I.1972 I.1972 I.1972 I.1972 I.1972 Aref="genomic DNA" Alignment Scores: 1.75e-183 Length: 1972 Score: 2015.00 Matches: 386 Percent Similarity: 98.0% Mismatches: 2 Best Local Similarity: 98.0% Mismatches: 2 Ouery Match: 2 Gaps: 1	US-10-733-816-2 (1-394) x BD181611 (1-1972)
reent Similarity: 98.0% Conservative: 0 st Local Similarity: 98.0% Conservative: 0 st Local Similarity: 98.0% Mismacches: 2 ery Match: 2 6.0% Mismacches: 2 7 Gludly Mismacches: 6 110.733-816-2 (1-394) x AR097211 (1-1972) 7 Gludly Glydly Mismacches: 1 110 GAAGGAAAAGGTGAATCGAGAAGGCCATCATGTCGGGGGGACCACACTTTT 21 AlaGluSerCyslysProValGlnGlnProSerAlaPheGlySerMetLysValSerArg	170 GCGGAGAGCTGCAGCGCAGCAGCTTCAGCTTTTGGTAGCATGAAAGTTAGCAGA 41 AspLysAapGlySerLysValThrThrValValAlaThrProGlyGlnGlyProAspArg 41 AspLysAapGlySerLysValThrThrValValAlaThrProGlyGlnGlyProAspArg 4230 GATAAAGATGGCACAAGGTAACCAGTGGTGGCAACTCCTGGACAGGTCCTGACAGG 61 ProGlnGluValSerTyrThrAspThrLysValI	10 AAGCGATTTAAGAACCGAGAGCTCCAGATCATGAGAAGCTGTAACATAGTC	Qy 181 TyrileHisSerPheGlyIleCysHisArgAspIleLysProGlnAsnLeuLeuLeuRsp 200	Db 830 GCCACCGATTACACGTCTAGTATAGATGTATGGCTCGCAGGCTGTGTGGCTGAATTG 889 Qy 261 LeuLeuGlyGlnProIlePheProGlyAspSerGlyValAspGlnLeuValGluIleIle 280 Db 890 TTGCTAGGACAACCAATATTTCCTGGGGACAGTGGTGGATTGGTGGTGGAATAATA 949 Qy 281 LysValLeuGlyThrProThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGlu 300 Db 950 AAGGTCCTAGGAACCAAATAGAGAAATAGAGAAATAATAGAAA 1009 Qy 301 PheLysPheProGlnIleLysAlaHisProTrpThrLysValPheArgProArgThrPro 320

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TyrGlnAlaLysLeuCysAspSerGlyGluLeuValAlaIleLysLysValLeuGlnAsp 100
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                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
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PACENTIC JP 199423983-A 1 30-AUG-1994;
MITSUBISHI KASEI CORP
OS Rattus Sp. (Tat)
PN 20 199423983-A/1
PP 30-AUG-1994
PF 03-AUG-1994
PI SHIGHEN KOICHI, SATO NAOTAKE, UCHID, PC COTK13/00,C12Q1/48/A61K37/56;
CC strandedness: Double;
CC strandedness: Double;
FH Key Linear;
FH Key / Corganism='Rattus sp. / Corganism='Rat
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/mol_type="genomic RNA"
/db_xref="taxon:10118"
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                                                                                                                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
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                                                                                   GlnThrLeuProVallleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla
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                             CCACAGGAAGTCAGTTACACAGACACTAAAGTCATTGGAAATGGGTCATTTGGTG
                                                                                                                                                                                                AAGCGATTTAAGAACCGAGAGCTCCAGATCATGAGAAAAGCTAGATCACTGTAACATAGTC
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ProGlnGluValSerTyrThrAspThrLysValIleGlyAsnGlySerPheGlyValVal
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1972 bp DNA encoding tau protein kinase I. E08007

LOCUS DEFINITION ACCESSION

470 CGATTGCGGTATTTCTTCTACTCGAGTGGCGAGAAGAAGATGAGGTCTACCTTAACCTG

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/ LTAIN 1 ALTON - "MSGRPRTTS PAES CKPVQQPSAFGSMKVSRDKDGSKVTTVVATP
GGOPDRAPGVSTTPTKVIGNS FGVYVQAKLOSBGELVALKKVLQDKFRKNRELQIMR
KLDHCNI VALLAY FFSGEKKDBVYLJALJALDYVPETVYRVAHYSBAKQTLEVI YVKL
YMYQLPRSLAY IHSFGICHRD I KPQNLLLDPDTAVLKLCDFGSAKQLVRGBPNVSYI C
STRYRAPEL I FGATDYTSSI IDVWSAFCYLAELLGQPP FFSDSGVDQLVBT I KVLGTP
TREQI REMNENYTERFPQI KAHPWTKVPRPRTPPRA I ALGSKLLEYTPTALIFLED
CAHSPPDELRDPNVKLPNGRDTPALFVETQELSSNPPLATILI PPHARI QAAASPPA
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Meb site:
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 120 Row: h Column: 7 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKerran, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Worllalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Roug, A.C., Shevchenko, Y.,
Bouffaxd, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (03-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/tissue type="Mammary tumor metastatized to lung.
MMTV-LTR/Wnt1 model. Expression driven by an MMTV-LTR
                                                                                                                                                                                                                                                                                                                                                     human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477§32
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/db_xref="GeneID:56637"
/db_xref="MG:1861437"
1453..2715
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/lab_host="DH10B"
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/strain="Czech II"
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausberg, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Parmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1010 TTCAAATTCCCCCAAATCAAGGCACATCCTTGGAAGGTCTTTGGGCCCCGAACTCCC 1069
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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                                              GTGCTGGACTATGTTCCGGAAACAGTGTACAGAGTCGCCAGACACTATAGTCGAGCCAAG
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Direct Submission
Submitted (13-JUL-2001) Yumiko Sano, National Institute of Advanced
Industrial Science and Technology (AIST), Research Center for
Glycoscience (RCG), Glycogene Function Team, Central-2 OSL, 1-1-1
Umezono, Tsukuba, Ibaraki, 305-8568, Japan
(B-mail:yumiko-sano@aist.go.jp, Tel:81-29-861-3197,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2443 CCACTGGAAGCTTGTGCACATTTTTTTTTTTTTTTTTGCGGGACCCAAATGTCAAACTA 2502
                                                                                                                                                                                                                                    ROD 15-JAN-2005
                                 ricaaariccercaaarcaagedacareceregacaaaggrericegeceegaacreea 2382
                                                                                                                                          ProLeuGluhlaCysAlaHisSerPhePheAspGluLeuArgAspProAsnValLysHis 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Burchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
PheLysPheProGlnIleLysAlaHisProTrpThrLysValPheArgProArgThrPro
                                                                       ProGluhlaIleAlaLeuCysSerArgLeuLeuGluTyrThrProThrAlaArgLeuThr
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                                                                                                                                                                                                                                                                                                           CCCCTCTGGCCACCATCCTTATCCCTCCACATGCTCGGATT 2604
                                                                                                                                                                                                                                                                                      381 ProProLeuAlaThrileLeuIleProProHisAlaArgile 394
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Organism="Mus musculus"

/mol type="mRNR"

/db_xref="taxon:10090"

1. 1612

/codon_start=1
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AB066114.1 GI:57834171
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Best Local Similarity:
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Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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                                         LysValLeuGlyThrProThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGlu
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                                                                                                                              ProGluAlaIleAlaLeuCysSerArgLeuLeuGluTyrThrProThrAlaArgLeuThr
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Method to modify differentiation of pluripotential
Patent: WO 03068961-A 42 21-AUG-2003;
Axordia Limited (GB)
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other sequences; artificial
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       ValileGlyAenGlySerPheGlyValValTyrGlnAlaLysLeuCysAepSerGlyGlu 90
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                                          CTGGTCGCCATCAAGAAAGTATTGCAGGACAAGAGATTTAAGAATCGAGAGCTCCCAGATC
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28 Holder,J.C.

AL Parent: WO 03000882-A 6 03-JAN-2003,

Parent: WO 03000882-A 6 03-JAN-2003,

SMITHKLINB BEBECHAM PLC (GB)

SMITHKLINB BEBECHAM PLC (GB)

1. 1263

1. 1263

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Coding nucleic acid sequence of the transgene used for the production of GSK-3 beta transgenic non-human animals" 110 CTGGTCGCCATCAAGAAAGTATTGCAGGACAAGAGATTTAAAGAATCGAGAGCTCCAGATC 300 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190 230 TCAGCTTTTGGCAGCATGAAAGTTAGCAGAGACAAGGACGGCAGCAAGGTGAACGTG MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrThrVal ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAonArgGluLeuGlnIle TATATGTATCAGCTGTTCCGAAGTTTAGCCTATATCCATTCCTTTGGAATCTGCCATCGG PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 1263 383 0 1 0 0 Length:
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            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Hell +49 30 32639 110

www.rzpd.de
This clone is available from RZPD;
This clone is available from RZPD;
This CDS clone is a part of a collection of human full ORF clones jointly established and verified by the Harvard Institute of proceedings and RZPD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGTCAGGGCGGCCCAGAACCACCTCCTTTGCGGAGAGCTGCAAGCCGGTGCAGCAGCCCT
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                                                                                                                                                                                                   This CDS has been cloned incl. stopcodon.

This CDS has been cloned incl. stopcodon.

The CDS has been cloned into pDONR201 via a BP Clonase (TM) reaction. Additional sequence has been added in front of the scodon: att. .AAAAA GCA GGC TCC ACC (ATG).

The stopcodon is followed by the 3' att site:

(stop) GACCCAGCTTTCTT. .att Compared to the reference sequence BO012760

we did not find any amino acid exchanges.
                                                                                                                                                                                                                                                                                                                                                             we did not find any amino acid exchanges.
Clone distribution: http://www.rzpd.de/products/orfclones/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RZPDo834A0920D"
/clone_lib="Human Full ORF Clones Gateway(TM)
/lab_host="DH10B"
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Mismatches:
Indels:
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Matches:
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1021 GATGAATTACGCGACCCAAATGTCAAACTACCAAATGGGCGAGACACACCTGCACTCTTC 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD0834A0920D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
                                                                                                                                                                                                                             781 AGTGGTGTGGGTGGGTAGAATAATCAAGGTCCTGGGAACTCCAACAAGGGAGCAA 840
                                                                                                                                                                                                                                                                                                                                                                                                            960
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                                                                                                                                                                                                                                                                                                                             900
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                                                                          661 TACTATAGGGCACCAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGTA 720
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg
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1 (bases 1 to 1263)

Halleck, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S., Koubert, P., Katrang, K., Schatten, R., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and LaBaer, J.

Cloning of human full open reading frames in Gateway (TM) system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry vector (pDONR201)
Unpublished
2 (bases 1 to 1263)
Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S., Neubert,P., Katrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
                                                                                                                                                                                       SerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGin
                                                                                                                                                                                                                                                                                                              TGGACTAAGGTCTTCCGACCCCGAACTCCACCGGAGGCAATTGCACTGTGTAGCGCGTCTG
TTTGGAAGTGCAAAGCAGCTGGTCCGAGGAGAACCCAATGTTTCGTATATCTGTTCTCGG
                                                                                                                TrpSerAlaGlyCysValLeuAlaGluLeuLeuLeuGlyGlnProIlePheProGlyAsp
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www.rzpd.de/products/orfclones/
                                      TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal
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CR536510
CR536510.1 GI:49168505
Full ORF shuttle clone, Gateway(TM), complete cds.
Homo sapiens (human)
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1141 CATGCTCGGATT 1152
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AUTHORS
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JOURNAL
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241 C	111 M 301 A		151 A 421 A					251 T 721 T	271 S 781 A		311 T 901 T				391 H
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ORGANISM: Homo sapiens
SEQ ID NO 2
LENGTH: 394
TYPE: PRT
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Sequence 16, Appl
Sequence 5, Appl
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Sequence 7, Appli
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Sequence 6, Appli
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Sequence 51997, A
Sequence 82945, A
Sequence 17, Appl
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Sequence 1, Appli
Sequence 10, Appl
Sequence 15, Appl
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Sequence 48109, A
Sequence 46581, A
Sequence 46580, A
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Sequence 4, Appli
Sequence 85, Appli
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Sequence 14, Appli
Sequence 12944, Appli
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Sequence 3
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          GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-733-816-1
US-11-299-324-10
US-11-299-324-18
US-11-299-324-18
US-10-733-816-5
US-10-733-816-5
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US-10-733-816-7
US-10-733-816-7
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US-10-953-349-33014
US-11-056-355B-13204
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Maximum Match 100%
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Sequence 33013, A Sequence 13203, A Sequence 4903, Ap Sequence 4904, Ap Sequence 52659, A Sequence 13205, A Sequence 5573, Ap Sequence 13502, A Sequence 5573, Ap Sequence 5573, Ap Sequence 12502, A Sequence 125
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US-11-056-3558-13559
US-11-056-3558-13569
US-11-056-3558-13569
US-11-056-3558-13569
US-11-056-3558-1369
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ALIGNMENTS

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PQEVSYIDIKVIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIV 120
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                                                                                      APPLICANT: Harrison, Stephen D.
APPLICANT: Hall, John A.
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Fang, Eric Y.
APPLICANT: Foot, Doris G.
APPLICANT: Madina-Selby, Angelica
TITLE OF INVENTION: GSK3 POLYBERTIDES
TITLE REFERENCE: 59516-162/PP-15876.002/200130.524
CURRENT APPLICATION NUMBER: US/10/713,816
CURRENT PILING DATE: 2003-12-10
FRIOR APPLICATION NUMBER: US/0/211,412
FRIOR APPLICATION NUMBER: US/0/211,412
FRIOR PILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FASELSEQ for Windows Version 4.0
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Sequence 2, Application US/10733816 Publication No. US20060088932A1 GENERAL INFORMATION:
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NFTTOELSSNPPLATILIPPHARI 394
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                                                                                ; Sequence 10, Application US/11299324; Publication No. US20060127388A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.7
Matches 383; Conservative
                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                US-11-299-324-10
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                                                                                                        301 FKFPQIKAHPWIKVFRPRIPPEAIALCSRLLEYTPTARLTPLEACAHSFFDELRDPNVKH 360
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APPLICANT: Zhong, Ziyang
APPLICANT: Fang, Eric Y.
APPLICANT: Nguyen, Steve H.
APPLICANT: Nguyen, Steve H.
APPLICANT: Nguyen, Steve H.
APPLICANT: Medina-Selby, Angelica
TITLE OF INVENTION: SSK3 POLYEPPIDES
FILE REFERENCE: 59516-162/PP-15876.002/200130.524
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: US/10/733,816
PRIOR PLING DATE: 2002-07-31
PRIOR PLING DATE: 2001-07-31
PRIOR PLING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 97.3%; Score 2024; DB 6; I
Best Local Similarity 100.0%; Pred. No. 8.5e-119;
Matches 384; Conservative 0; Mismatches 0;
                                                                                                                                                                     361 PNGRDTPALFNFTTQELSSNPPLATILIPPHARI 394
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APPLICANT: Hall, John A.
APPLICANT: Calderon-Cacia, Maria
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TYPE: PRT
CRGANISM: Homo sapiens
US-10-733-816-1
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Sequence 15, Application US/11299324
Publication No. US20060127388A1
GENERAL IMPORMATION:
APPLICANT: Cain, Michael
APPLICANT: Cain, Michael
APPLICANT: Cain, Wichael
TITLE OF INVERTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof
TITLE OF INVERTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof
TITLE OF INVERTION: Variants of Glycogen Synthase Cinase 3 and Uses Thereof
CURRENT APPLICATION UNMBER: US/11/299,324
CURRENT FILING DATE: 2005-12-09
PRIOR FILING DATE: 2004-12-10
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.3
SEQ ID NO 15
APPLICANT: Cain, Michael
APPLICANT: Yaworsky, Paul J
IITLE OF INVENTION 'Variants of Glycogen Synthase Kinase 3 and Uses Thereof
FILE REPERBNCE: WYE-052
CURRENT PILITAGO DATE: 2005-12-09
PRIOR APPLICATION NUMBER: US 60/634,813
PRIOR APPLICATION NUMBER: US 60/634,813
PRIOR PILING DATE: 2004-12-10
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.3
SEQ ID NO 10
LENGTH: 420
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99.7%; Pred. No. 4.1e-118;
iive 0; Mismatches 1;
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RESULT 6

US-11-209-324-18

Sequence 18, Application US/11299324

Publication No. US20060127388A1

GENERAL INFORMATION:

APPLICANT: Cain, Michael

TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof

TITLE OF INVENTION: UNDER: US/11/299,324

CURRENT FILING DATE: 2005-12-09

PRIOR FILING DATE: 2005-12-09

PRIOR FILING DATE: 2004-12-10

NUMBER OF SEQ ID NOS: 44

SEQ ID NO 18

LENTH: 387

LENTH: 387
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NFTTODANT 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQIKAHP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG 130
                                                                                                                                                                                                                                                                    71 VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG 130
                                                                                                                                                                                                                                                                                                                                                         EKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLAYIHSFGICHR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 WSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQIKAHP 300
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                                                                                                   Length 433;
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US-11-283-329-216
| Sequence 216, Application US/11283329
| Publication No. US20060134670A1
| GENERAL INFORMATION:
| APPLICANT: Piu, Fabrice
| TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS |
| TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS |
| CURRENT FILING DATE: 2005-11-18 |
| PRIOR APPLICATION NUMBER: 60/629,811 |
| PRIOR PILING DATE: 2004-11-19 |
| NUMBER OF SEQ ID NOS: 242 |
| SEQ ID NO 216 |
| SEQ ID NO 216
                                                                                                                                             1; Indels
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Pred. No. 4.5e-117;
0; Mismatches 1;
                                                                                                     Score 1996.5; DB 7
Pred. No. 4.5e-117;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.9%;
                                                                                                     Query Match
Best Local Similarity 96.5%;
Matches 383; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 96.5
Matches 383; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CORGANISM: Homo sapiens
US-11-283-329-216
                          TYPE: PRT
ORGANISM: Homo sapiens
                                               ; ORGANISM: Hom
US-11-299-324-15
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ORGANISM: Homo sapiens
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APPLICANT: Cain, Michael
APPLICANT: Yaworsky, Paul J
TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof
FILE REFERENCE: WE-052
CURRENT APPLICATION NUMBER: US/11/299,324
CURRENT FILING DATE: 2005-12-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PQEVSYTDTKVIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 RLRYFFYSSGEKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLRYFFYSSGEKKDEVXLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YIHSFGICHRDIKPQNLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 361;
                                                                                                            APPLICANT: Calderon-Cacia, Maria
APPLICANT: Zhong, Ziyang
APPLICANT: Zhong, Ziyang
APPLICANT: Pang, Earc Y.
APPLICANT: Pang, Earc Y.
APPLICANT: Nguyen, Steve H.
APPLICANT: Nguyen, Steve H.
APPLICANT: Medina-Selby, Angelica
ITLE OF INVENTION: GSK3 POLYPEPTIDES
FILE REPERENCE: 59516-162/PP-15876.002/200130.524
CURRENT APPLICATION NUMBER: US/10/733,816
CURRENT PILING DATE: 2003-12-10
PRIOR FILING DATE: 2002-07-31
PRIOR FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 11
SOTTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
90.5%; Score 1883.5; DB 6
Best Local Similarity 91.6%; Pred. No. 3.9e-110;
Matches 361; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PNGRDTPALFNFTTQELSSNPPLATILIPPHARI 394
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, Sequence 16, Application US/11299324
, Publication No. US20060127388A1
; GENERAL INFORMATION:
/ Sequence 3, Application US/10733816
/ Publication No. US20060088932A1
/ GENERAL INFORMATION:
                                                                    APPLICANT: Harrison, Stephen D. APPLICANT: Hall, John A. APPLICANT: Calderon-Cacia, Maria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 DIKPONLLLDPDTAVLKLCDPGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 WSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQIKAHP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 WTKVFRPRTPPEAIALCSRLLEYTPTARLTPLEACAHSFFDELRDPNVKHPNGRDTPALF 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 EKKDEUYLNLVLDYVPETUYRVARHYSRAKQTLPVIYVKLYMYQLFRSLAYIHSFGICHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 DIKPQNLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV
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                                                                                                                                                                                                                                                                                                                                                           32;
                                                                                                                                                                                                                                                                                                    Length 388;
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                                                                                                                                                                                                                                                                                                                                                        Indels
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APPLICANT: Harrison, Stephen D.
APPLICANT: Hall, John A.
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Zhong, Ziyang
APPLICANT: Zhong, Ziyang
APPLICANT: Pang, Eric Y.
APPLICANT: Media Selby, Angelica
TITLE OF INVENTION: GSK3 POLYPEPTIDES
TITLE OF INVENTION NUMBER: US/10/733,816
CURRENT APPLICATION NUMBER: US/10/711,412
PRIOR FILING DATE: 2002-07-31
PRIOR FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 WSAGCVLAELLLGQPIFPGDSGVDQLVEII-------
                                                                                                                                                                                                                                                                                             Query Match 86.9%; Score 1808; DB 7;
Best Local Similarity 91.4%; Pred. No. 2.1e-105;
Matches 351; Conservative 0; Mismatches 1;
PRIOR APPLICATION NUMBER: US 60/634,813
PRIOR FILING DATE: 2004-12-10
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 16
LENGTH: 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329 NFTTQELSSNPPLATILIPPHARI 352
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Publication No. US20060088932A1
GENERAL INFORMATION:
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300 SIDVWSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQI 359
                                                                                                                                                                                                                                                                   360 KAHPWTKVFKSRTPPEAIALCSSLLEYTPSSRLSPLEACAHSFFDELKCLGTQLPNNRPL 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 YSSGEKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLAYIHSFG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360 KAHPWTKVFKSRTPPEAIALCSSLLEYTPSSRLSPLEACAHSFFDELRCLGTQLPNNRPL 419
                                                                                                                                                                                                                                            307 KAHPWTKVFRPRTPPEAIALCSRLLEYTPTARLTPLEACAHSFFDELRDPNVKHPNGRDT 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 YSSGEKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLAYIHSFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIDVWSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQI
                        180 YSSGEKKDELYINLVLEYVPETVYRVARHFTKAKLTIPILYVKVYMYQLFRSLAYHSQG
                                                                                                                                                             SIDVWSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 TDTKVIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 ICHRDIKPONLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bodian. Dale
APPLICANT: Bodian. Sherif
APPLICANT: Daouti, Sherif
APPLICANT: Latario, Brian
APPLICANT: Latario, Brian
APPLICANT: Cuintavalla, Joseph
TITLE OF INVENTION: High throughput functional genomic
TITLE OF INVENTION: Screening methods for osteoarthritis
FILE REFERENCE: 4-33178
FILE REFERENCE: 2005-10-14
FILE REPERENT APPLICATION NUMBER: 00/463,933
FRIOR APPLICATION NUMBER: 60/463,933
FRIOR PLING DATE: 2003-04-18
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                              446
                                                                                                                                                                                                                                                                                                                         367 PALFNFTTQELSSNPPLATILIPPHAR 393
                                                                                                                                                                                                                                                                                                                                                Sequence 85, Application US/10553520; Publication No. US20060188885A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 483
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-553-520-85
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US-10-553-520-85
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                                                                                                                                                                 73 GGGGSGGPGAGTSFPPP------GVKLGR--DSGKVTTVVATLGQGPERSQEVAY
                                                                                                                                                                                                                         YSSGEKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLAYIHSFG
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                                                                8 GGGMSGRPRT-TSFAESCKPVQQPSAFGSMKVSRDKDGSKVTTVVATPGQGPDRPQEVSY
                             Gaps
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; Pred. No. 6e-93;
24; Mismatches 37; Indels 14;
                             14;
Pred. No. 5.6e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Harrison, Stephen D.
APPLICANT: Hall, John A.
APPLICANT: Hall, John A.
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Chong, Ziyang
APPLICANT: Fang, Eric Y.
APPLICANT: Coit, Doris G.
APPLICANT: Nguyen, Steve H.
APPLICANT: Nguyen, Steve H.
TITLE OF INVENTION: GSK3 POLYPEPTIDES
FILE REFERENCE: 59516-162/PP-15976.002/200130.524
                          24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/733,816
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: US/10/211,412
PRIOR FILING DATE: 2002-07-31
PRIOR FILING DATE: 2001-07-25
NUMBER: OF SEQ ID NOS: 11
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PALFNFTTQELSSNPPLATILIPPHAR 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10733816 Publication No. US20060088932A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.3%;
80.6%;
        80.68;
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Best Local Similarity 80.67
Matches 312; Conservative
      Best Local Similarity 80.6
Matches 312; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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US-11-299-324-14

Sequence 14, Application US/11299324

Sequence 14, Application US/11299324

Sequence 14, Application US/11299324

Sequence 14, Application US/11299324

GENERAL INFORMATION: US-20060127388A1

APPLICANT: Cain, Michael

APPLICANT: Yaworsky, Paul J

TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof

FILE REFERENCE: WYE-052

CURRENT APPLICATION NUMBER: US/11/299,324

CURRENT FILING DATE: 2005-12-09

PRIOR PELLING DATE: 2004-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 KVTTVVATPGQGPDRPQEVSYTDTKVIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 IYVKLYMYQLFRSIAYIHSFGICHRDIKPQNLLLDPDTAVLKLCDFGSAKQLVRGEPNVS 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 YICSRYYRAPELIFGATDYTSSIDVWSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGT 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
APPLICANT: Cott. Doris G.
APPLICANT: Cott. Doris G.
APPLICANT: Nguyen, Steve H.
APPLICANT: Nguyen, Steve H.
TITLE OF INVENTION: GSK3 POLYPEPTIDES
FILE REFERENCE: 59516-162/PP-15876.002/200130.524
CURRENT APPLICATION NUMBER: US/10/733,816
CURRENT APPLICATION NUMBER: US/10/211,412
PRIOR PILING DATE: 2002-07-31
PRIOR PILING DATE: 2002-07-31
PRIOR PILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO6
SEQ ID NO6: LENGTH: 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 76.3%; Score 1588; DB 6; Best Local Similarity 86.2%; Pred. No. 9.7e-92; Matches 300; Conservative 22; Mismatches 26;
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SOFTWARE: Patentin version 3.3
SEQ ID NO 14
ISNGTH: 278
TYPE: PRT
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US-11-299-324-14
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86.2%; Pred. No. 8.8e-92;
tive 22; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zhong, Ziyang
APPLICANT: Zhong, Ziyang
APPLICANT: Zhong, Ziyang
APPLICANT: Colt, Dorla G.
APPLICANT: Ocolt, Dorla G.
APPLICANT: Nguyen, Steve H.
APPLICANT: Medina-Selby, Angelica
TITLE OF INVENTION: GSK3 POLYEPTIDES
FILE REFERENCE: 59516-162/PP-15976.002/200130.524
CURRENT FILING DATE: 2003-12-10
PRIOR PLILNG DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US/10/211,412
PRIOR PLILNG DATE: 2002-07-31
PRIOR APPLICATION NUMBER: US/09/916,109
PRIOR PLING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FRAESEQ for Windows Version 4.0
           367 PALFNFTTQELSSNPPLATILIPPHAR 393
                                                           420 PPLFNFSAGELSIOPSLNAILIPPHLR 446
                                                                                                                                                                                         Sequence 7, Application US/10733816; Publication No. US20060088932A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Harrison, Stephen D.
APPLICANT: Hall, John A.
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Zhong, Ziyang
                                                                                                                                                                                                                                                                                                       Hall, John A.
Calderon-Cacia, Maria
                                                                                                                                                                                                                                                                                APPLICANT: Harrison, Stephen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 76.3%;
Best Local Similarity 86.2%;
Matches 300; Conservative
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ORGANISM: Homo sapiens
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US-10-733-816-6
                                                                                                                                            RESULT 12
US-10-733-816-7
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Publication No. US2006015028341
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Sequence Determined Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 82944
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                                                                                                                                                                                EKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLAYIHSFGICHR 180
                                                                                                                                                                                                                                                    VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG 130
                                                                                                                                                           EKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLAYIHSFGICHR 190
                                                                                                                                                                                                                                   DIKPQNLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 250
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                                     1 MSGRPRITSFAESCKPVQQPSAFGSMKVSRDKDGSKVTTVVATPGQEPDRPQEVSYTDTK
                  MSGRPRITSFAESCKPVQQPSAFGSMKVSRDKDGSKVITVVATPGQGPDRPQEVSYTDTK
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; LOCATION: (1)..(399)
; OTHER INFORMATION: Ceres Seq. ID no. 12668003
US-11-056-355B-82944
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 65.89
Matches 248; Conservative
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US-11-056-355B-82944
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Db 315 RTPPEAVDLVSRLLQYSPNIRSTAMEAIVHPFFDELRDPNTRLPNGRALPPLFNFKPQEL 374

QY 378 -SSNPPLATILIPPHAR 393

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Db 375 KGASLELLSKLIPDHAR 391

Search completed: September 15, 2006, 17:28:44

Job time: 36 secs
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301 FKFPQIKAHPWTKVFRPRTPPEAIALCSRLLEYTPTARLTPLEACAHSFFDELRDPNVKH 360
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-: /BMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
-: /BMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
-: /BMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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              GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-278-759-7
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US-10-689-461-1
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Calderon-Cacia, Maria
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61 PQEVSYTDTKVIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIV 120
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                                                 PNGRDTPALFNFTTQELSSNPPLATILIPPHARI 394
                                                                                                                                                                                                          APPLICANT: Harrison, Stephen D.
APPLICANT: Hall, John A.
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Zhong, Ziyang
APPLICANT: Zhong, Ziyang
APPLICANT: Pang, Eric Y.
APPLICANT: Ponyen, Steve H.
APPLICANT: Medina-Selby, Angelica
TITLE OF INVENTION: GSK3 POLYPEPTIDES
FILE REFERENCE: PP-15876.064/200130.524D1
CURRENT APPLICATION NUMBER: US/10/211,412A
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                 ; Sequence 2, Application US/10211412A; Publication No. US20030077798A1; GENERAL INFORMATION:
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Matches 394; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-211-412A-2
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US-10-689-461-2
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Sequence 2, Application US/10689461; Publication No. US20050048511A1; GENERAL INFORMATION: APPLICANT: Harrison, Stephen D. APPLICANT: Harrison, A.

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APPLICANT: Zhong, Ziyang
APPLICANT: Zhong, Ziyang
APPLICANT: Fang, Eric Y.
APPLICANT: Colt, Donis G.
APPLICANT: Nguyen, Steve H.
APPLICANT: Mguyen, Steve H.
APPLICANT: Medina-Selby, Angelica
TITLE OF INVENTION: GSK3 POLYPEPIDES
TITLE REPERBNCE: 59516-162/PP-15876.002/200130.524
CURRENT FILING DATE: 2002-10-20
PRIOR APPLICATION NUMBER: US/10/211,412
PRIOR PLING DATE: 2002-07-31
PRIOR APPLICATION NUMBER: US/9/916,109
PRIOR PLING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PRAESEQ for Windows Version 4.0
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US-10-689-461-2
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Sequence 7, Application US/10278759
; Publication No US20030114382A1
; GENERAL INFORMATION:
; APPLICANT: Walsh, Kenneth
; TILE OF INVENTION: Glycogen Synthase Kinase Function in Endothelial Cells
; FILE REFERENCE: 501237.70020.US
; FILE REFERENCE: 2002-10-23
; CURRENT PILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/350160
; PRIOR APPLICATION NUMBER: US 60/337905
; RILNG DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 7
; LENGTH: 420
                                                                                        241 WSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQIKAHP 300
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VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG
                    61 VIGNGSFGVVYQAKLCDSGELVAIKKVIQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG
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                                                                                                                                           DIKPONLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV
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Best Local Similarity 100.0%; Pred. No. 3e-164;
Matches 384; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
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US-10-278-759-7
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                                                                                                                        97.3%; Score 2024; DB 3;
100.0%; Pred. No. 3e-164;
iive 0; Mismatches 0;
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APPLICANT: Calderon-Cacia, Maria
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Pang, Eric Y.
APPLICANT: Pang, Eric Y.
APPLICANT: Mayorn, Steve H.
APPLICANT: Medina-Selby, Angelica
TITLE OF INVENTION: GSK3 POLYPEPTIDES
FILE REPERENCE: PP-15876.004/200130.524D1
CURRENT APPLICATION NUMBER: US/10/211,412A
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 420
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                                                                                                                        Query Match 97.3
Best Local Similarity 100.
Matches 384; Conservative
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ORGANISM: Homo sapiens
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                                                                  , ORGANISM: Homo
US-09-916-109-1
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                                 LENGTH: 420
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Matches 384
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HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630, 21472, 17692, 19290, 21620, 28899, 53659, 64549, 9465, 23544, 7366, 27447, 57259, 21844, 943, 2061, 5891, 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947, 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
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TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 819

TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 53659, 64

TITLE OF INVENTION: 9465, 23544, 7366, 27417, 27529, 23844, 28469, 3895, 1711E OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27844, 28469, 3895, 1711E OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 71TLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 71TLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 71TLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 71TLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 71TLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 71TLE OF INVENTION: 53003, 9205, 60448, 389

PRIOR PELING DATE: 2003-02-05

PRIOR PILING DATE: 2003-03-03-05

PRIOR PILING DATE: 2003-04-03

PRIOR PILING DATE: 2003-05-13

PRIOR PILING DATE: 2003-05-13

PRIOR PILING DATE: 2003-05-13

PRIOR PILING DATE: 2003-09-15

PRIOR PILING DATE: 2003-09-10-10

PRIOR PILING PAPILCATION NUMBER: US 60/510,351

PRIOR PILING PAPILCATION PRIOR PAPILCATION PAPILCATION PAPILCATION PAPILCATION PAPILCATION PAPILC
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100.0%; Pred. No. 3e-164;
iive 0; Mismatches 0;
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; ORGANISM: Homo sapiens
US-10-772-636-72
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US-10-689-461-1
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                      301 WIKVFRPRIPPEAIALCSRLLEYTPTARLIFLEACAHSFFDELRDPNVKHPNGRDTPALF 360
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US-10-772-636-72

Sequence 72, Application US/10772636

Sequence 72, Application US/10772636

SENERAL INFORMATION:
APPLICANT: Kelly, Louise M.
APPLICANT: Carroll, Joseph M.
APPLICANT: Heally, Aileen
APPLICANT: Heally, Aileen
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/10482524

| Bublication No. US20040261137A1
| GENERAL INFORMATION:
| APPLICANT: Smithkline Beecham PLC |
| APPLICANT: Smithkline Beecham PLC |
| TILLE OF INVENTION: Models for Metabolic Disorders |
| FILE REPERBUGE: PG4458 |
| CURRENT APPLICATION NUMBER: US/10/482,524 |
| CURRENT PILING DATE: 2003-12-22 |
| PRIOR FILING DATE: 2001-06-26 |
| PRIOR FILING DATE: 2001-06-26 |
| PRIOR FILING DATE: 2001-06-36 |
| PRIOR FILING DATE: 2001-06-36 |
| SOFTWARE: Patentin Ver. 2.1 |
| TENGRAPH OF THE PATENT OF THE 
                                                                                                                                  361 NFTTQELSSNPPLATILIPPHARI 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NFTTQELSSNPPLATILIPPHARI 394
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US-10-482-524-4
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PRIOR FILING DATE: 2002-10-23
PRIOR FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: PCT/GB02/04780
PRIOR APPLICATION NUMBER: GB 0126506.5
PRIOR FILING DATE: 2001-11-05
PRIOR FILING DATE: 2001-11-27
PRIOR FILING DATE: 2001-11-27
PRIOR FILING DATE: 2002-02-11
NUMBER OF SEQ ID NOS: 306
SOFTWARE: PARENTIN VERSION 3.1
SEQ ID NO 257
LENGTH: 420
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; Publication No. US20060078947A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
US-10-840-060-257
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US-11-288-493-72
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Publication No. US20050227243A1

GENERAL INFORMATION:
APPLICANT: Cyclacel Limited
APPLICANT: Frenz, Lisa
APPLICANT: Frenz, Lisa
APPLICANT: Midgley, Carol
TITLE OF INVENTION: Call Cycle Progression Proteins
FILE REFERENCE: 10069/2012
CURRENT APPLICATION NUMBER: US/10/840,060
                                                              APPLICANT: Harrison, Stephen D.
APPLICANT: Hall, John A.
APPLICANT: Hall, John A.
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Zhong, Ziyang
APPLICANT: Zhong, Ziyang
APPLICANT: Chit, Doris G.
APPLICANT: Rang, Eric Y.
APPLICANT: Medina-Selby, Angelica
TITLE OF INVENTION: GSK3 POLYPEPTIDES
FILE REFERENCE: 59516-162/PP-15876.002/200130.524
CURRENT APPLICATION NUMBER: US/10/689,461
CURRENT FILING DATE: 2003-10-20
PRIOR APPLICATION NUMBER: US/10/211,412
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100.0%; Pred. No. 3e-164;
tive 0; Mismatches 0;
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No. US20050048511A1
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ORGANISM: Homo sapiens
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APPLICANT: Kelly, Louise M.
APPLICANT: Kelly, Louise M.
APPLICANT: Carroll, Joseph M.
APPLICANT: Carroll, Joseph M.
APPLICANT: Carroll, Joseph M.
APPLICANT: Tearlow, Deborah
TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,
TITLE OF INVENTION: 1472, 17622, 19290, 21689, 21689, 53659, 64549,
TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5891,
TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27844, 28469, 38947,
TITLE OF INVENTION: 5014
TITLE OF INVENTION NUMBER: US/11/288,493
CURRENT APPLICATION NUMBER: US/10/772,636
PRIOR APPLICATION NUMBER: US 60/445,241
PRIOR FILING DATE: 2003-02-05
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Query Match 97.3%; Score 2024; DB 5; Length 420; Best Local Similarity 100.0%; Pred. No. 3e-164; Matches 384; Conservative 0; Mismatches 0; Indels
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371 NFTTQELSSNPPLATILIPPHARI 394
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              SOFTWARE: PatentIn version 3.2
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Best Local Similarity 99.77
Matches 383; Conservative
                            ; SEQ ID NO 31
; LENGTH: 414
; TYPE: PRT
; ORGANTSM: Homo sapiens
US-10-746-545-31
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LENGTH: 420
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US-10-278-759-6
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PRIOR APPLICATION NUMBER: US 60/448,389
PRIOR PILING DATE: 2003-02-18
PRIOR PLILING DATE: 2003-02-18
PRIOR PLILING DATE: 2003-03-20
PRIOR PILING DATE: 2003-03-20
PRIOR PILING DATE: 2003-04-03
PRIOR PILING DATE: 2003-04-03
PRIOR PILING DATE: 2003-04-03
PRIOR PILING DATE: 2003-04-03
PRIOR PILING DATE: 2003-05-13
PRIOR PILING DATE: 2003-05-13
PRIOR PILING DATE: 2003-05-13
PRIOR PILING DATE: 2003-05-13
PRIOR PILING DATE: 2003-05-04-06
PRIOR PILING DATE: 2003-09-06
PRIOR PILING DATE: 2003-09-05
PRIOR APPLICATION NUMBER: US 60/502,909
PRIOR PRIOR APPLICATION DATE: 2003-09-05
PRIOR PILING DATE: 2003-09-05
PRIOR PILING DATE: 2003-09-05
PRIOR PRIOR APPLICATION NUMBER: US 60/502,909
PRIOR PRIOR APPLICATION NUMBER: US 60/502,909
PRIOR PRIOR APPLICATION NUMBER: US 60/502,909
PRIOR PRIOR DATE: 2003-09-05
PRIOR PRIOR APPLICATION NUMBER: US 60/502,909
PRIOR PRIOR DATE: 2003-09-05
PRIOR PRIOR DATE: 2003-09-05
PRIOR DATE: 2003-09-09-09
PRIOR DATE: 2003-09-09-09-09
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100.0%; Pred. No. 3e-164;
iive 0; Mismatches 0; Indels
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; Publication Wo. US20040171075A1
; Publication Wo. US20040171075A1
; GENERAL INFORMATION:
    APPLICANT: Perillo.
    APPLICANT: Petillo. Peter A
; TILLE OF INVENTION: MODULATION OF PROTEIN FUNCTIONALITIES
; FILE REFERENCE: 34475
; CURRENT APPLICATION WHERE: US/10/746,545
; CURRENT PILING DATE: 2002-12-24
; PRIOR APPLICATION WHERE: 2002-12-24
; RIOR PILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 38
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Best Local Similarity
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US-10-746-545-31
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TITLE OF INVENTION: Glycogen Synthase Kinase Function in Endothelial Cells
FILE REPERENCE: 801237.70020.05
CURRENT APPLICATION NUMBER: US/10/278,759
CURRENT FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: US 60/350160
PRIOR APPLICATION NUMBER: US 60/337905
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-11-13
SUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
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     Length 414;
                                                    Indels
Query Match 96.7%; Score 2013; DB 4; Best Local Similarity 99.7%; Pred. No. 2.5e-163; Matches 383; Conservative 0; Mismatches 1;
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61 VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG 120
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US-10-746-545-15
US-10-746-545-15
Sequence 15, Application US/10746545
Publication No. US2004017075A1
GENERAL INFORMATION:
APPLICANT: Plyn. Daniel L.
APPLICANT: Petillo, Peter A.
TITLE OP INVENTION: MODULATION OF PROTEIN FUNCTIONALITIES
FILE REPERENCE: 34475
CURRENT APPLICATION NUMBER: US/10/746,545
CURRENT FILING DATE: 2003-12-24
FRIOR APPLICATION NUMBER: US 60/437,487
FRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.2
SEQ ID NO 15
SEQ ID NO 15
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Pred. No. 2.6e-163;
0; Mismatches 1;
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                                                                          371 NFTTOELSSNPPLATILIPPHARI 394
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Best Local Similarity 99.7%;
Matches 383; Conservative (
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CRGANISM: Homo sapiens
US-10-746-545-15
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; Publication No. US20030125332A1
; Sequence 1, Application No. US20030125332A1
; GENERAL INFORMATION:
APPLICANT: TER HAAR, ERNST
; APPLICANT: GREEN, USCHAEL J.
TITLE OF INVENTION: INHIBITORS OF GSK-3 AND CRYSTAL STRUCTURES OF GSK-3B
; TITLE OF INVENTION: PROTEIN AND PROTEIN COMPLEXES
; TITLE OF INVENTION: UNMERR: US/10/135,255
; CURRENT APPLICATION NUMBER: US/10/135,255
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/297,094
; PRIOR PILING DATE: 2001-06-08
; PRIOR FILING DATE: 2001-06-08
; PRIOR FILING DATE: 2001-06-08
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS.
; SOFTWARE: PATENTIN VÜET: 2.1
; SEG ID NO 1.
   DIKPONLLLDPDTAVLKLCDFGSAKOLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 240
                                                                                                WSAGCVLAELLIGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQIKAHP 300
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Pred. No. 2.6e-163;
0; Mismatches 1;
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Best Local Similarity 99.7
Matches 383; Conservative
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, ORGANISM: Homo sapiens
US-10-135-255-1
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US-10-135-255-1
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1 MEYMPWEGGGMSGRPRTTSF.....QELSSNPPLATILIPPHARI 394
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/BMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
/BMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
/BMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
/BMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-336-038-1

US-09-316-1038-1

US-09-316-1038-1

US-09-538-092-1163

US-09-916-109-5

US-09-916-109-5

US-09-916-109-5

US-09-916-109-5

US-09-916-109-6

US-10-211-412B-7

US-09-916-109-6

US-09-538-092-1162

US-09-538-092-1162

US-09-916-109-6

US-10-211-412B-7

US-09-916-109-6

US-10-211-412B-7

US-09-916-109-6

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Maximum DB seq
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			Length Indels	MEYMPMEGGGMSGRPRITSFAESCKFVQQPSAFGSMKVSRDKDGSKVTTVVATPGGGPDR 	POBUSYIDIKVIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIV 	RIRYFFYSSGEKKDEVYLAUVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLA
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US-00-00-00-00-00-00-00-00-00-00-00-00-00	~	1-2 6465231 CORMATION: Harrison, Stephen D. Harrison, Stephen D. Hall, John A. Calderon-Cada, Maria Zhong, Ziyang Fang, Bric Y. Coit, Doris G. Wguyen, Steve H. Medina-Selby, Angelica NVEWTION: GSK2 POLYEPTIDES IENCE: PP-15876.002/200130.5; SEQ ID NOS: 11 FastSEQ for Windows Version 194 Homo sapiens HOME 1-2	, S. 1, 0, 1	SFAES SFAES	\$ - - - - - - - - - - - - - - - - - - -	
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22266666666666444444444446666666666666		RESULT 1 US-09-916-109-2 Sequence 2, Application US/09916109 Patent No. 6465231 GENERAL INFORMATION: APPLICANT: Harrison, Stephen D. APPLICANT: Calderon-Cacia, Maria APPLICANT: Calderon-Cacia, Maria APPLICANT: Calderon-Cacia, Maria APPLICANT: Coit, Doris G. APPLICANT: Mayon, Sive H. APPLICANT: Madina-Selby, Angelica TITLE OF INVERTION: GSK3 POLYPEPTIDES FILE REFERENCE: PP-15876.002/200130.5 CURRENT APPLICATION UNDER: US/09/916 CURRENT FILING DATE: 2001-07-25 NUMBER OF SEQ ID NOS: 11 SOFTWARE: FREEERQ for Windows Version SOFTWARE: PRT TYPE: PRT TYPE: PRT CORGANISM: Homo sapiens	Query Match Best Local Matches 39			
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LENGTH: 420
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APPLICANT: Harison, Stephen D.
APPLICANT: Harison, Stephen D.
APPLICANT: Caldaron-Cacia, Maria
APPLICANT: Caldaron-Cacia, Maria
APPLICANT: Caldaron-Cacia, Maria
APPLICANT: Colt. Doris G.
APPLICANT: Cott. Doris G.
APPLICANT: Nguyen, Steve H.
APPLICANT: Mquyen, Steve H.
APPLICANT: SSC JO 10 11, 412B
CURRENT APPLICATION NUMBER: USO9/916, 109
PRIOR FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 11
SCTUMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2.
TENENT APPLICANTON NUMBER: DATE APPLICANTON AP
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ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 394; Conservative
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US-10-211-412B-2
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US-09-336-038-1; Sequence 1, Application US/09336038; ; Patent No. 6417185

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APPLICANT: Goff, Dane
APPLICANT: Goff, Dane
APPLICANT: Harrison, Steven
APPLICANT: Harrison, Steven
APPLICANT: Ring, David B.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Inhibitors of Glycogen Synthase Kinase 3
TITLE OF INVENTION: Inhibitors of Glycogen Synthase Kinase 3
TITLE OF INVENTION: Inhibitors of Glycogen Synthase Kinase 3
TITLE OF INVENTION: INHORER: US/09/336,038
CURRENT APPLICATION NUMBER: 60/089,978
EARLIER FILING DATE: 1998-06-19
NUMBER OF SEQ ID NOS: 4
SOFFWARE: PATENTIN Ver. 2.0
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97.3%; Score 2024; DB 2; Length 420;
Best Local Similarity 100.0%; Pred. No. 6.9e-215;
Matches 384; Conservative 0; Mismatches 0; Indels
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Sequence 1, Application US/09916109
GENERAL INPORMATION:
APPLICANT: Harrison, Stephen D.
APPLICANT: Galdenon-Cacia, Maria
APPLICANT: Zhong, Ziyang
APPLICANT: Coct, Doris G.
APPLICANT: Rang, Eric Y.
APPLICANT: Rong, Eric Y.
APPLICANT: Rong, Steve H.
APPLICANT: Mquyen, Steve H.
APPLICANT: Solit Mquyen, Steve H.
APPLICANT: Mquyen, 
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ORGANISM: Homo sapiens
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  71 VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG 130
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Sequence 1163, Application US/09538092

Patent No. 6753314

GENERALI INORMATION:

APPLICANT: Giot. Loic

APPLICANT: Giot. Loic

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

FILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR PILING DATE: 1999-04-01

PRIOR PILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SEQ ID NOS: 1387

SEQ ID NO 1163
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                                      61 VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKORELQIMRKLDHCNIVRLRYFFYSSG
                                                                                                              131 EKKÜBÜYLINLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYOLFRSLAYIHSFGICHR
                                                                                                                                                                                                                                DIKPQNLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV
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100.0%; Pred. No. 6.9e-215;
tive 0; Mismatches 0; Indels
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; OTHER INFORMATION: Polypeptide Accession Number P49841
US-09-538-092-1163
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Best Local Similarity 100.0
Matches 384; Conservative
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NAME/KEY: misc_feature
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US-09-538-092-1163
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100.0%; Pred. No. 6.9e-215;
iive 0; Mismatches 0; Indels
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APPLICANT: Zhong, Ziyang
'APPLICANT: Zhong, Ziyang
'APPLICANT: Coit, Doris G.
APPLICANT: Coit, Doris G.
APPLICANT: Mquyen, Steve H.
APPLI
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Best Local Similarity 100.0%; Pred. No. 6.9e-215;
Matches 384; Conservative 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6716624
GENERAL INFORMATION:
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Calderon-Cacia, Maria
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                                                                                                                                                                 Best Local Similarity 100.
Matches 384; Conservative
                       TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-10-211-412B-1
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                                                           ; ORGANISM: HOUS-09-1
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WSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEPKFPQIKAHP 310
                                                                                                                                                                 WSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTBFKFPQIKAHP 300
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                                                                                   DIKPONLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV
                                                            DIKPONLLLDPDTAVLKLCDPGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV
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91.6%; Pred. No. 1.9e-199;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NGUVEN, Steve H.
APPLICANT: Medina-Selby, Angelica
TITLE OF INVENTION: GSK2 POLYBEPTIDES
FILE REPERRINCE: PP-15876.002/200130.524
CURRENT APPLICATION NUMBER: US/09/916,109
CURRENT FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 11
SCOFTWARE: FASISEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                  NFTTQELSSNPPLATILIPPHARE 394
                                                                                                                                                                                                                                                                                                                             1 MEYMPMEGGG------
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Patent No. 6465231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Harrison, Stephen D. APPLICANT: Hall, John A. APPLICANT: Calderon-Cacia, Maria
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Matches 361, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zhong, Ziyang
APPLICANT: Fang, Eric Y.
APPLICANT: Coit, Doris G.
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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Patent No. 5837853
GENERAL INFORMATION:
ARABINOS.
APPLICANT: AKIAIKO TAKASHIMA et al.
TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE
TITLE OF INVENTION: CAL-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG 130
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  301 WIKVFRPRTPPEAIALCSRLLEYTPTARLTPLEACAHSFPDELRDPNVKHPNGRDTPALF 360
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                                                              WIKVFRPRIPPEAIALCSRLLEYTPIARLTPLEACAHSFFDELRDPNVKHPNGRDTPALF
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96.6%; Score 2010; DB 1; Length 420;
Best Local Similarity 99.5%; Pred. No. 2.5e-213;
Matches 382; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTRY: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 144 mb
COMPUTER: 18M COMPALIDE
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,264A
PILING DATE: February 20, 1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/204,091
FILING DATE: March 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REPERENCE/DOCKET NUMBER:
TELECOMMUNICATION:
                                                                                                                                                                 NFTTQELSSNPPLATILIPPHARI 394
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SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: amino acid
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TOPOLOGY: linear
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ORIGINAL SOURCE:
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US-08-602-264A-14
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367 PALFNFTTQELSSNPPLATILIPPHAR 393
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Patent No. 6716624
GENERAL INFORMATION:
APPLICANT: Harrison, Stephen D.
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APPLICANT: Calderon-Cacia, Maria
APPLICANT: Zhong, Ziyang
APPLICANT: Fang, Eric Y.
APPLICANT: Coit, Doris G.
Zhong, Ziyang
Fang, Eric Y.
Coit, Doris G.
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US-10-211-412B-5
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APPLICANT: Zhong, Ziyang
APPLICANT: Fang, Eric Y.
APPLICANT: Coit, Doris G.
APPLICANT: Mguyen, Steve H.
APPLICANT: Mguyen, Steve H.
APPLICANT: Mguyen, Steve H.
APPLICANT: Mguyen, Steve H.
APPLICANT: Mgina-Selby, Angelica
FILE REFERENCE: 5916-162/PP-15876.002/200130.524
CURRENT APPLICATION NUMBER: US/10/211,412B
CURRENT FILING DATE: 2002-07-31
PRIOR PILLING DATE: 2001-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 90.5%; Score 1883.5; DB 2; Best Local Similarity 91.6%; Pred. No. 1.9e-199; Matches 361; Conservative 0; Mismatches 0;
    361 PNGRDTPALFNFTTQELSSNPPLATILIPPHARI 394
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                            328 PNGRDTPALFNFTTQELSSNPPLATILIPPHARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                             Sequence 3, Application US/10211412B
Patent No. 6716624
GENERAL INFORMATION:
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Patent No. 6465231
GENERAL INFORMATION:
APPLICANT: Harrison, Stephen D.
APPLICANT: Hall, John A.
APPLICANT: Calderon-Cacia, Maria
                                                                                                                                                                                                             APPLICANT: Harrison, Stephen D.
APPLICANT: Hall, John A.
APPLICANT: Calderon-Cacia, Maria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-10-211-412B-3
                                                                                                                              US-10-211-412B-3
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LENGTH: 361
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US-09-916-109-5
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APPLICANT:
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APPLICANT: Medina-Selby, Angelica
TITLE OF INVENTION: GSK3 POLYPEPTIDES
FILE REPERRANCE: 59516-162/PP-15876.002/200130.524
CURRENT APPLICATION NUMBER: US/10/211,412B
CURRENT FILING DATE: 2002-07-31
PRIOR PPLICATION NUMBER: US09/916,109
PRIOR PILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 5: SEQ ID NO 5: 11
                                                                                                                                                                                                                                                                                                                                                                                Query Match

77.3%; Score 1609; DB 2;
Best Local Similarity 80.6%; Pred. No. 6.7e-169;
Matches 312; Conservative 24; Mismatches 37;
APPLICANT: Nguyen, Steve H.
APPLICANT: Medina-Selby, Angelica
TITLE OF INVENTION: GSK1 POLYPEPTIDES
FILE REFERENCE: PP-15876.002/200130.524
CURRENT APPLICATION NUMBER: US/09/916,109
CURRENT FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FRALSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 447
FYPE: PRT
ORGANISM: Homo sapiens
US-09-916-109-5
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180 YSSGEKKDELYLALVLEYVPETVYRVARHFTKAKLTIPILYVKVYMYQLFRSLAYIHSQG 239
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APPLICANT: Harrison, Stephen D.
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Zhong, Ziyang
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Colt, Doris G.
APPLICANT: Nguyen, Steve H.
APPLICANT: Medina-Selby, Angelica
CURRENT APPLICATION NUMBER: US/10/211,412B
CURRENT FILING DATE: 2002-07-31
PRICR PILING DATE: 2001-07-25
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SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 483
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US-10-211-412B-4
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                                                               77.3%; Score 1609; DB 2; Length 447; 80.6%; Pred. No. 6.7e-169; ive 24; Mismatches 37; Indels 1.
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GRNEAL INFORMATION:
APPLICANT: Harrison, Stephen D.
APPLICANT: Harrison, Stephen D.
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Zhong, Ziyang
APPLICANT: Cold, Dorls G.
APPLICANT: Colt, Dorls G.
APPLICANT: Rang, Eric Y.
APPLICANT: Media-Selby, Angelica
ITLE REPERENCE: PP-15876.002/20130.524
CURRENT FILING DATE: 2001-07-25
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                                                                                     Best Local Similarity 80.6
Matches 312; Conservative
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    ORGANISM: Homo sapiens
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Best Local Similarity
Matches 312; Conservat
                        US-10-211-412B-5
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US-09-916-109-4
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 KAHPWTKVFRPRTPPEAIALCSRLLEYTPTARLTPLEACAHSPFDELRDPNVKHPNGRDT 366
                    360 KAHPWTKVFKSRTPPEAIALCSSLLEYTPSSRLSPLEACAHSFFDELRCLGTQLPNNRPL 419
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Patent No. 675314

GENERAL INFORMATION:

APPLICANT: Glot, Loid

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REPRENCE: 15966-54

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT PILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR PILING DATE: 1999-04-01

PRIOR FILING DATE: 2000-02-01

PRIOR FILING DATE: 2000-02-01

PRIOR FILING DATE: 2000-02-01

PRIOR FILING DATE: 2000-02-01

SOFTWARE: CURPARES: CURPARES: 60/178,965

SEQ ID NO 1162

LENGTH: 483
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CTHER INFORMATION: Polypeptide Accession Number P49840
US-09-538-092-1162
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80.6%; Pred. No. 7.6e-169;
tive 24; Mismatches 37;
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Best Local Similarity 80.69
Matches 312; Conservative
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US-09-538-092-1162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 PIREQIREMNDNYTEPKFPQIKAHPWTKVFKSRTPPEAIALCSSLLEYTPSSRLSPLEAC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 KVTTVVATPGQGPDRPQEVSYIDTKVIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 KVTTVVATLGQGPERSQEVAYTDIKVIGNGSFGVVYQARLAETRELVAIKKVLQDKRFKN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 PTREQIREMNPNYTEFKFPQIKAHPWTKVFRPRTPPEAIALCSRLLEYTPTARLTPLEAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 IYVKLYMYQLFRSLAYIHSFGICHRDIKPQNLLLDPDTAVLKLCDFGSAKQLVRGEPNVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 76.3%; Score 1588; DB 2; Best Local Similarity 86.2%; Pred. No. 9.5e-167; Matches 300; Conservative 22; Mismatches 26;
APPLICANT: Harrison, Stephen D.
APPLICANT: Harrison, Stephen D.
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Zhong, Ziyang
APPLICANT: Coit, Doris G.
APPLICANT: Mayen, Steve H.
APPLICANT: Medina-Salby, Angelica
APPLICANT: Medina-Salby, Angelica
APPLICANT: Medina-Salby, Angelica
APPLICANT: Medina-Salby, Angelica
APPLICANT: WINDER: US/09/916,109
CURRENT FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SSO_ID NO.
LENGTH: 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Homo sapiens
US-09-916-109-7
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Search completed: September 15, 2006, 17:13:51 Job time : 52 secs

RESULT 15 US-09-916-109-7 Sequence 7, Application US/09916109 ; Patent No. 6465231

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GenCore version 5.1.9
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OM protein - protein search, using sw model

September 15, 2006, 17:04:00; Search time 302 Seconds (without alignments) 1206.808 Million cell updates/sec Run on:

US-10-733-816-2 Perfect score:

2081 1 MEYMPWEGGGMSGRPRITSF......QBLSSNPPLATILIPPHARI 394 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

2849598 seqs, 925015592 residues Searched:

2849598 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ption	homo sapien		homo sapien	m glycogen	rattus norv	spermophilu		brachydanio	xenopus lae	xenopus lae	tetraodon n	brachydanio	brachydanio	ciona intes	lytechinus	paracentrot	homo sapien	rattus norv	tetraodon n	homo sapien	anopheles g	drosophila	suberites d	hydra atten	dugesia jap	caenorh	caenorhabdi	caenorhabdi	drosophila	ustilago ma	nothinia hish
Description	P49841	09wv60	Q6f127	Q5kn03	P18266	Q5yjc2	09ibd2	09yh60	091757	091627	Q480h0	Q9yh61	O9ipd3	Q9n143	Q6ing5	046150	P49840	P18265	Q4ssg6	068d16	Q7qa46	P18431	Q4h118	Q9gtk0	Q58982	Q9y0c2	Q9u2q9	05wnk0	P83101	Q4ph53	20000
SUMMAKIES	GSK3B HUMAN	GSK3B_MOUSE	Q6F127 HUMAN	Q5KU03 MOUSE	GSK3B RAT	QSYJCZ SPECI	Q9IBD2_BRARE	Q9YH60_BRARE	Q91757_XENLA	Q91627 XENLA	Q4SOHO TETNG	Q9YH61_BRARE	Q9IBD3_BRARE	Q9NL43_CIOIN	Q6IUG5_LYTVA	046150_PARLI	GSK3A HUMAN	GSK3A RAT	Q4SSG6_TETNG	Q68D16_HUMAN	Q7QA46 ANOGA	SGG DROME	Q4H118 SUBDO	Q9GTK0 HYDAT	Q589S2_DUGJA	Q9Y0C2_CAEEL	Q9U2Q9_CAEEL	Q5WNK0 CAEBR	GSK3H DROME	Q4PH53 USTMA	VUTTO SOON
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* Query Match Length	420	420	420	420	420	420	421	421	420	420	496	440	435	407	414	414	483	483	399	388	363	1067	443	442	431	362	362	359	501	402	400
% Query Match	96.7	96.7	96.7	96.7	96.6	96.4	94.1	94.1	92.8	92.4	86.2	81.9	80.2	80.1	78.4	77.6	77.3	77.2	77.2	76.6	75.2	74.1	71.9	71.4	69.3	64.6	64.5	64.5	62.7	62.6	62
Score	2013	2013	2013	2013	2010	2006	1959	1959	1931	1923	1793.5	1704.5	1669.5	1666.5	1632	1614	1609	1607	1606	1594	1565	1542.5	1495.5	1485	1443	1343.5	1342.5	1341.5	1305.5	1302	1206
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NUCLEOTIDE SEQUENCE OF 1-28.

physcomitre	cryptococcu			nicotiana t						aspergillus			
Q6vm07	Q55x64			024139						Q5ayx2		082038	Q6vm10
Q6VM07 PHYPA	Q55X64 CRYNE	Q5KMR8 CRYNE	KSG5 ARATH	024139 TOBAC	Q6VM11_PHYPA	O82029_TOBAC	Q6EUS4 ORYSA	Q6VM08 PHYPA	Q4WDL1_ASPFU	Q5AYX2 EMENI	Q6AVQ3 ORYSA	O82038 PETHY	Q6VM10_PHYPA
N	N	~	Н	N	N	~	~	0	~	~	7	~	7
423	398	398	410	471	424	471	401	423	412	394	424	470	355
62.2	62.0	62.0	61.7	61.3	61.2	61.2	61.2	61.1	61.0	60.7	60.7	60.7	9.09
1294	1289.5	1289.5	1283	1275.5	1273.5	1273.5	1273	1271	1269	1264	1263.5	1262.5	1262

ALIGNMENTS

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TISSUB-EPAP, and Placenta;

XI TISSUB-EPAP, and Placenta;

XI TISSUB-EPAP, and Placenta;

XI Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Rrausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Derge J.G., Brachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., N., Norley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska M.A.;

""Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE (ISOFORM 1).
MEDLINE=95071278; PubMed=7980435;
Stambolic V., Woodgett J.R.;
"Mitogen inactivation of glycogen synthase kinase-3 beta in intact cells via serine 9 phosphorylation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhoads A.R., Karkera J.D., Detera-Wadleigh S.D.; "Radiation hybrid mapping of genes in the lithium-sensitive wnt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99455114; PubMed=10523816; DOI=10.1038/sj.mp.4000538;
                                    P49841, OSBWH3; OSBWH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE OF 185-202.
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STANDARD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
GSK3B HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse
HERET TRANSPORTED TO THE PROPERTY OF THE PROPE
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Event=Alternative splicing; Named isoforms=2;

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MEDLINEs99417672; PubMed=10486203; DOI=10.1006/geno.1999.5875; Lau K.F., Miller C.C.J., Anderton B.H., Shaw P.C.; "Moleoular cloning and characterization of the human glycogen synthase kinase-2beta promoter."; Genomics 60:121-128(1999).
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HBU H.-C., Lee Y.-L., Cheng T.-S., Howng S.-L., Chang L.-K., Lu P.-J.,
Hong Y.-R.;
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PubMed=15302935; DOI=10.1073/pnas.0404720101;
Beaucoleil S.A., Jedrychowski M., Schwartz D., Elias J.E., Villen J.,
Li J., Cohn M.A., Cantley L.C., Gygi S.P.,
"Large-scale characterization of Hela cell nuclear phosphoproteins.";
Proc. Natl. Acad. Sci. U.S.A. 101:12130-12135(2004).
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PubMed=15592455; DOI=10.1038/nbt1046;
Rush J., Moritz A., Lee K.A., Goos V.L., Spek E.J., Zhang H.,
Zha X.-M., Polakiewicz R.D., Comb M.J.;
"Immunoaffinity profiling of tyrosine phosphorylation in cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Characterization of two non-testis-specific CABYR variants that bind
                                                                                                         CHARACTERIZATION.
CHARACTERIZATION.
CHARACTERIZATION.
DOI-10.1073/pnas.95.19.11211;
Delcommenne M. Tan C., Gray V., Rue L., Woodgett J.R., Dedhar S.;
"Phosphoinositide-3-OH kinase-dependent regulation of glycogen synthase kinase 3 and protein kinase B/AKT by the integrin-linked
                                                                                                                                                                                                                                                                                                                            Cloning and characterization of a novel human ninein protein that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 27-393 OF PHOSPHORYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7Z6N3:UPF3A; NDEXp=1; IntAct=EBI-373586, EBI-372587; ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to GSK3beta with a proline-rich extensin-like domain."; Biochem. Biophys. Res. Commun. 329:1108-1117(2005).
                                                                                                                                                                                                                                                                                                                                                 interacts with the glycogen synthase kinase 3beta.";
Biochim. Biophys. Acta 1492:513-516(2000).
                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 95:11211-11216(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 35-386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nat. Biotechnol. 23:94-101(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERACTION WITH GSK3B.
                                                                                                                                                                                                                                                        INTERACTION WITH NIN.
                                                                                                                                                                                                                                                                                                                 Howing S.-L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cells."
                                                                                                                                                                                                       kinase.
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MIM; 605004; gene.

R LinkHub; P49841;

CO; GO:0004596; F:glycogen synthase kinase 3 activity; TAS.

GO; GO:0005515; F:procein binding; IPI.

R GO; GO:000557; F:glycogen metabolism; TAS.

R InterPro; IPR000219; Prot kinase.

R InterPro; IPR001299; Ser_thr_pkinase.

R InterPro; IPR001299; Ser_thr_pkinase.

R InterPro; IPR001245; Tyr. pkinase.

R InterPro; IPR001245; Tyr. pkinase.

R R ROSITE; PS00100; Prot kinase; 1.

R SWART; SM00200; STKC; 1.

R ROSITE; PS00101; PROTEIN KINASE ATP; 1.

R PROSITE; PS00101; PROTEIN KINASE ST; 1.

R PROSITE; PS00109; PROTEIN KINASE ST; 1.

W Nucleotide binding; Phosphorylation; Serine/threonine-protein kinase; m read-ferrace. Whi etching the strong the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                         Note=No experimental confirmation available,
-- TISSUE SPECIFICITY: Expressed in testis, thymus, prostate and
ovary and weakly expressed in lung, brain and kidney.
-- PTM: Phosphorylated by AKT1 and ILK1.
-- SIMILARITY: Belongs to the Ser/Thr protein kinase family. GSK-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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/FIId=PRO 0000085980.
Protein Kinase.
ATP (By similarity).
ATP (By similarity).
ATP (By similarity).
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/FTId=VSP_004790.
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Phosphoserine (By similarity).
Phosphothreonine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphoserine (by PKB/AKT1).
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V -> G (in Ref. 4)
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BC012760; AAH12760.1; -; mRNA.
AF098789; AAC69340.1; -; Genomic_DNA.
AR074333; AAD48517.1; -; Genomic_DNA.
SS3324; SS3324.
                                                                                                                                          IsoId=P49841-2; Sequence=VSP_004790;
Name=1;
IsoId=P49841-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ensembl; ENSGG000082701; Homo sapiens.
H-InvDB; HIX0003589; -.
HGNC; HGNC:4617; GSK3B.
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                                                                                                                           VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFPYSSG 130
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                                                                                                                                                                                                                                       WIKVERPRIPPEAJALCSRLLEYTPTARLIPLEACAHSFPDELRDPNVKLPNGRDTPALF 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE MENA].

STRAIN=Czech II, and FVB/N; TISSUE=Mammary gland;
MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnss.242603899;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Heich F.,
B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hoich F.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B Townstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubzratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                                                          EKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLAYIHSFGICHR 190
                                                                                                                                                                                                                         DIKPONLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 250
                                                                                                                                                                                                                                                                       WSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQIKAHP 310
                                                                                                                                                                                                                                                                                    WIKVERPRIPPEALALCSRLLEYTPTARLTPLEACAHSFFDELRDPNVKHPNGRDTPALF 370
                                                                               11 MSGRPRTISFAESCKPVQQPSAFGSMKVSRDKDGSKVTTVVATPGQGPDRPQEVSYTDTK 70
                                                                                                     MSGRPRITSFAESCKPVQQPSAFGSMKVSRDKDGSKVTIVVAIPGQGPDRPQEVSYIDIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salameh W.A., Guo T.B., Chan K.C., Mitchell A.P.; Tresticular expression and hormonal control of glycogen synthase kinase 3, a homologue of Salar RIM11. Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                        ö
                                 Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAR-2006, entry version 52.
Glycogen synthase kinase-3 beta (EC 2.7.1.37) (GSK-3 beta).
Name-Gsk3b;
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2000, integrated into UniProtKB/Swiss-Prot
                                                        ;
                                Score 2013; DB 1;
Pred. No. 4.1e-148;
0; Mismatches 1;
L -> H (in Ref. 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                 96.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [MRNA].
                                           Local Similarity 99.7
Les 383; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cells.";
Nat. Biotechnol. 23:94-101(2005).
-!- FUNCTION: Participates in the Wnt signaling pathway. Implicated in the hormonal control of several regulatory proteins including glycogen synthase, MYB and the transcription factor JUN (By

    Similarity).
    CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
    SUBUNT: Monomer. Interacts with NIN (By similarity).
    PTM: Phosphorylation on Tyr-216 is necessary for the activity (By

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CHAIN 1420 Glycogen synthase kinase-3 beta.

PTIGE-PRO 0000085981.

PTO PROTEIN S6 340 Protein kinase.

NP BIND 62 70 ATP (By similarity).
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-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. GSK-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=15592455; DOI=10.1038/nbt1046; Rush., Woritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang Zha X.-M., Polakiewicz R.D., Comb M.J.; "Immunoaffinity profiling of tyrosine phosphorylation in cancer
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R G010005829; C:CYCOS01; IDA.

R G05 G00005634; C:Mucleus; IDA.

R G05 G00005634; C:Mucleus; IDA.

R G05 G00008013; F:Deta-catenin binding; IPI.

R G05 G00008013; F:Deta-catenin binding; IPI.

R G05 G00008213; F:Call profein kinase activity; IDA.

R G05 G00008214; F:Call proliferation; TAS.

R G05 G00008283; P:Call proliferation; TAS.

R G05 G00008284; P:Call proliferation; IDA.

R G05 G00006468; P:Protein amino acid phosphorylation; IDA.

R G05 G00000311; P:Protein amino acid phosphorylation; IDA.

R G05 G00000320; P:re-entry into mitotic cell cycle; IDA.

R G05 G00000320; P:re-entry into mitotic cell cycle; IDA.

R G05 G00000320; P:re-entry into mitotic cell cycle; IDA.

R G05 G00000320; P:re-entry into mitotic cell cycle; IDA.

R G05 G00000320; P:re-entry into mitotic cell cycle; IDA.

R InterPro: IPR000290; Ser_thr_pkin_AS.

R InterPro: IPR0012945; TYP. pkinase.

R InterPro: PF001295; TYP. pkinase.
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SMART; SM0220; S_TKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS5011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=15345747; DOI=10.1074/mcp.M400085-MCP200; Ballif B.A., Villen J., Beausoleil S.A., Schwartz D., Gyg "Phosphoproteomic analysis of the developing mouse brain. Mol. Cell. Proteomics 3:1093-1101(2004).
                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION SITE SER-389, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION SITE TYR-216, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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EMBL; BC006936; AAH06936.1; -; mRNA.
EMBL; BC060743; AAH60743.1; -; mRNA.
HSSP; P49841; 1GNG.
                                                                                                                                                                                                                                                         and mouse cDNA sequences."
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SMR; Q9WV60; 23-386.
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InterPro; IPR008271; Ser_thr_pkin AS.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001295; Ter_thr_pkinase.
InterPro; IPR001295; Ter_pkinase.
Pfam; PP00069; Phinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROFIEIN KINASE DOM; 1.
PROSITE; PS00107; PROFIEIN KINASE DOM; 1.
PROSITE; PS00108; PROFIEIN KINASE ST; 1.
ATP-binding; Kinase; Nucleotide-Dinding;
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InterPro; IPR000719; Prot_kinase
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QSKU03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #TKVFRPRIPPEAIALCSRLLEYIPTARLTPLEACAHSFFDELRDPNVKLPNGRDTPALF 360
                                                                                                                                                                                                                                                                                                                            WSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQIKAHP 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                          MSGRPRTTSFAESCKPVQQPSAFGSMKVSRDKDGSKVTTVVATPGQGPDRPQEVSYTDTK
                                                                                                                                                                                                                                                                                                     VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG
                                                                                                                                                                                                                                                                                                                                                                                   EKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLAYIHSFGICHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIKPQNLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV
                                                                                                                                                                                                                       11 MSGRPRITSFAESCKPVQQPSAFGSMKVSRDKDGSKVITVVATPGQGPDRPQEVSYIDIK
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GO:000166; F:nucleotide binding; IEA.
GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO:0016740; F:protein aerine; IEA.
GO:0016740; F:protein amino acid phosphorylation; IEA.
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-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
                   PKB/AKT1) (By
                                                                                                                                       Length 420;
                                                                                                                                                                             1; Indels
                                                                                                   CRC64;
                                                                                                                                                     Pred. No. 4.1e-148;
0; Mismatches 1;
(By similarity)
                                                                              Phosphoserine.
200C3FD1B38B4883
                                                                                                                                           Score 2013; DB 1;
                     Phosphoserine (by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QFI27 HUMAN PRELIMINARY; PRT; 420 AA. 06F127; 10-MAY-2005, integrated into UniProtKB/TrEMBL. 10-MAY-2005, sequence version 1. 07-FEB-2006, entry version 9.
                                                         Phosphotyrosine.
                                      similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ensembl; ENSG0000082701; Homo sapiens.
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Q6F127; 23-386.
                                                                                                   46710 MW;
                                                                                                                                     96.7%;
                                                                                                                                                                               Matches 383; Conservative
                                                      216
389
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                                                                                                 420 AA;
                                                                                                                                                            Local Similarity
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10-MAY-2005, sequence version 1.
10-MAY-2005, sequence version 1.
10-MAY-2005, sequence version 1.
10-MAY-2005, sequence version 1.
10-MAY-2005, sequence nerry kinase 3 beta/cau protein kinase I (NOD-derived CDIIC +ve dendritic cells cDNA, RIKEN full-length enriched library, clone: F630213P21 product: glycogen synthase kinase 3 beta, full insert sequence) (NOD-derived CDIIC +ve dendritic cells cDNA, RIKEN full-length enriched library, clone: F630015008 product: glycogen synthase kinase 3 beta, full insert sequence).
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                      Gaps
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Imahori K.;
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
Serine/threconine-protein kinase; Transferase.
SEQUENCE 420 AA; 46744 MW; 4ACC24D00CDBB9C3 CRC64;
                                                                                                                                        Pred. No. 4.1e-148;
0; Mismatches 1;
                                                                                                          96.7%; Score 2013; DB 2; 99.7%; Pred. No. 4.1e-148;
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RAY Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., RA Garninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., RA Garninci P., Kasukawa T., Lenhard B., Wells C., Kodzius R., Shimokawa K., RA Gais W.J., Wilming L.G., Aldinis V., Allen J.E., Savolan M., Davis M.J., Wilming L.G., Aldinis V., Allen J.E., Savolan M., Annesi-Impionato A., Apweller R., Aturaliya R.M., Balley T.L., RA manesi-Impionato A., Apweller R., Aturaliya R.M., Banter L. Beisel K.W., Bersano T., Bono H., Chalk A.M., Crow M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G., Fletcher C.F., Putushina T., Furuno M., Futakis S., Garibodi M., Recorgii-Hemming P., Gingeras T.R., Cagiobori T., Green R.E. Gustincich S., Harbers M., Katoh M., Kavasawa Y., Kelso J., Kitamura H., Jaku M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Jaku M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Juni S., McWilliam S., Madana Babu M., Madera M., Marchfonni L., Juni S., McWilliam S., Madana Babu M., Madera M., Marchfonni L., Liu J., Liuni S., McWilliam S., Maindan Babu M., Madera M., Marchfonni L., Sheng Y., Ranapiu-Tabar S., Mulder N., Nakano N., Nakauchi H., Nigono R., Mishiawa S., Nori F., Ohara O., Estuya B., Ruan Y., Salzberg S., Sandellar R., Schneider C., Pervan W.J., Pavesi G., Person S., Sessa L., Sheng Y., Shimada Y., Shimada K., Sluya B., Sinclair B., Stuyka E., Sugiuca K., Senjo S., Sessa L., Sheng Y., Tammoja K., Tan S.L., Tang S., Tang K., Waller R., Waller W., Bult C., Mattick J., Tang S., Tang R., Manlestedt C., Mattick J.S., Hume D.A., Kal C., Yagi K., Wallenia T., Kawagashira N., Teadada R., Nathero K., Sulakan M., Suzuki M., Machol J., Arakawa T., Fukuda S., Kamanishi H., Kawasalama T., Suzuki M., Nakashima T., Suzuki S., Nakashima T., Suzuki W., Nakashima T., Suzuki W., Nakashima T., Suzuki W., Nakashima T., Suzuki W., Nakashi J., Nakashima T., Suzuki W., Nakashima T., Suzuki W., Nakashima T., Suzuki W., Nakashi J., 
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X MEDLINE-23154681; POI=10.1038/nature01266;
A Nikaldo I., Osaton M., Kasukawa T., Adachi J., Bono H., Kondo S.,
A Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T.,
A Radi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T.,
A Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
A Blake J.A., Braapin A., Matsuda H., Batalov S., Beisel K.W.,
A Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
A Gaaterland T., Gariboldi M., Gissi C., Godzik A., Frazer K.S.,
A Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
A Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
A Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
                               MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium; "Antisense Transcription in the Mammalian Transcriptome."; science 309:1564-1566 (2005).
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                                                                                                                                             PubMed=16141072; DOI=10.1126/science.1112014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=16141073; DOI=10.1126/science.1112009;
                                              Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Methods Enzymol. 303:19-44(1999).
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                       "Molecular cloning and expression of glycogen synthase kinase-3/factor
            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                     WUCLEOTIDE SEQUENCE [WRNA].
STRAIN=Sprague-Dawley, TISSUE-Brain cortex;
MEDLINE=93307488; PubMed=768508; DOI=10.1016/0014-5793(93)81066-9;
MEDLINE=93307488; PubMed=768508; DOI=10.1016/0014-5793(93)81066-9;
Ishiquro K., Shirateuchi A., Sato S., Omori A., Arioka M.,
Kobayashi S., Uchida T., Imahori K.;
"Glycogen synthase Kinase 3 beta is identical to tau protein kinase generating several epitopes of paired helical filaments.";
FEBS Lett. 325:167-172(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REMBL; X53428; CAA37519.1; -; mRNA.

REMBL; X73553; CAA52020.1; -; mRNA.

REMBL; X35428; CAA52020.1; -; mRNA.

REMBL; X91941; 1109.

REMBL; S14709; TURTO.

SMR; P18266; 23-386.

REMBL; S182NGO0000002833; Rattus norvegicus.

REMBL; 70982; GRASD.

ROJ; G0:0004696; F:glycogen synthase kinase 3 activity; IDA.

GO; G0:0005515; F:procein binding; IDA.

ROJ; G0:0005517; P:procein binding; IDA.

ROJ; G0:0006917; P:induction of apoptosis; IDA.

ROJ; G0:0006917; P:induction of apoptosis; IDA.

ROJ; G0:0006917; P:induction of transcription, DNA-d...;

RICEPPO; IPR008271; Ser_thr_pkinase.

RICEPPO; IPR001245; Tyr_pkinase.

REPPO; PR0001245; Tyr_pkinase.

REPPO; PR0001245; Tyr_pkinase.
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R PROSITE; PROSILI, KINASE ATP; 1.

R PROSITE; PSO010; PROTEIN KINASE ATP; 1.

R PROSITE; PSO0108; PROTEIN KINASE DOM; 1.

R PROSITE; PSO0108; PROTEIN KINASE DOM; 1.

R PROSITE; PSO0108; PROTEIN KINASE ST; 1.

R ATP-binding; Kinase; Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase; Transferase; Wnt signaling pathw Serine/threonine-protein kinase; Transferase; Wnt signaling pathw CHAIN 56 340 Protein kinase.

I DOMAIN 56 340 Protein kinase.

I NP BIND 62 70 ATP (By similarity).

I ACT SITE 181 181 Proten acceptor (By similarity).

I BINDING 85 87 ATP (By similarity).

I MOD_RES 9 Phosphoserine (by PKB/AKT1) (By
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Hughes K., Nikolakaki E., Plyte S.E., Totty N.F., Woodgett J.R.;
"Modulation of the glycogen synthase kinase-3 family by tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bimilarity)
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MEDLINE-90316097; Pubmed=2164470;
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                                                                                                                                                                        NUCLEOTIDE SEQUENCE [MRNA].
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Rattus norvegicus (Rat).
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Glycogen synthase kinase-3 beta (EC 2.7.1.37) (GSK-3 beta) (Factor A) (FA).
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Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases
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ENER, DSXU03; 23-386.

Ensembl; ENSWUSGO000022812; Mus musculus.

MGI: B61437; G8K3b.

GO; GO:0005839; C:0vtlosol; IDA.

GO; GO:0005839; C:nvcleus; IDA.

GO; GO:000813; F:beta-cateain binding; IPI.

GO; GO:0006913; F:tau-protein kinase activity; IDA.

GO; GO:0006918; P:ant-apoptosis; IMP.

GO; GO:0008918; P:att-apoptosis; IMP.

GO; GO:0008918; P:att cell differentiation; IDA.
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Best Local Similarity 99.7%; Pred. No. 4.1e-148;
Matches 383; Conservative 0; Mismatches 1;
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EMBL, AK170965; BAE42146.1; -; MENA.
EMBL; AK154293; BAE32494.1; -; MRNA.
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GGK3B RAT
LD GGK3B RAT
AC P18266;
DT 01-NOV-1990, 1
DT 07-MAR-2096, e
DE GJyCOGEN BYNCH
DE (GRA).
                                                                               STRAIN-NOD;
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EMBL; AB032265; BAA92442.1; -; mRNA.
HSSP; P49841; 1109.
  InterPro; IPR001245; Tyr pkinase
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GO; GO: 0005524; F:ATP binding; IEA.
GO; GO: 0000166; F:nucleotide binding; IEA.
GO; GO: 0001674; F:protein serine/threonine kinase activity; IEA.
GO; GO: 0016740; F:transferase activity; IEA.
GO; GO: 0016740; F:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR000219; Ser_thr_pkin.AS.
InterPro; IPR002290; Ser_thr_pkin.ase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
                                                                                   Length 420;
               Phosphoserine (By similarity).
Y->F: Loss of phosphorylation.
M -> V (in Ref. 2).
2F473FCAB89B4398 CRC64;
                                                                                                             Indels
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                                                                                  Score 2010; DB 1;
Pred. No. 7.1e-148;
    Phosphotyrosine.
                                                                                                             1; Mismatches
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                                                        46742 MW;
                                                                                96.6%;
99.5%;
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tches 382; Conservative
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SEQUENCE
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Distributed under the Creative Commons Attribution-NoDerivs License
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MEDLINE=20171051; PubMed=10704853; DOI=10.1016/S0925-4773(99)00319-6; Shimizu T., Yamanaka Y., Ryu S.-L., Hashimoto H., Yabe T., Hirano T., Bae Y.-K., Hibl M., Hirano T.; Coperative roles of Bozozok/Dharma and Nodal-related proteins in the formation of the dorsal organizer in zebrafish,"; Mech. Dev. 91:293-303(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                               Length 420;
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Pfam; PF00069; PKinase; 1.

Prodom; PR000001; Prot Kinase; 1.

PROSTIE; SM00220; ETKC; 1.

PROSTIE; PS500110; PROTEIN KINASE ATP; 1.

PROSTIE; PS00108; PROTEIN KINASE DOM; 1.

PROSTIE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Nucleotide-binding; Serine/threonine-protein kinase; Transferase.

SEQUENCE 420 AA; 46744 MW; 5F5243CA7D9EA549 CRC64;
                                                                                                                                                                                                                                                                                                           Score 2006; DB 2;
Pred. No. 1.5e-147;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000, sequence version 1. 07-FBB-2006, entry version 26. Glycogen synthase kinase 3 beta.
                                                                                                                                                                                                                                                                                                                  96.4%;
99.5%;
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.5'
Matches 382; Conservative
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Differential expression of glycogen synthase kinase 3 genes during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371 NETTOELSSNPPLATILIPPHAR 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 NFTTOELSSNPTLASILIPAHAR 383
                                                                                                                                                                                                                                                                                                  EMBL; AJ223502; CAA11420.1; -; mRNA.
HSSP: P49841; 1109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                   zebrafish embryogenesis.";
Mech. Dev. 91:387-391(2000)
                                                                                                                                                                                                                                                                                                                                             P49841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q91757 XENLA
Q91757;
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ID Q91757 XI
AC Q91757;
DT 01-NOV-19
DT 07-PEB-2D
INTracell
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       셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WSAGCVLABLLLLGQPIPPGDSGVDQLVBIIKVLGTPTREQIREMNPNYTEFKFPQIKAHP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQIRAHP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WIKVFRPRIPPEALALCSRLLEYTPTARLTPLEACAHSFFDELRDPNVKHPNGRDTPALF 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIGNGS FGVVYQAKLCDSGELVAIKKVLQDKR FKNRELQIMRKLDHCNIVRLRYFFYSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIKPONLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV
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MEDLINE=20171069; Pubmed=10704871; DOI=10.1016/S0925-4773(99)00300-7;
Tsai J.N., Lee C.H., Jeng H., Chi W.K., Chang W.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OgyH60.

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94.1%; Score 1959; DB 2;
Best Local Similarity 96.9%; Pred. No. 6.7e-144;
Matches 371; Conservative 7; Mismatches 5.
                                           ENSDARG00000017803; Danio rerio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NFTTOELSSNPPLATILIPPHAR 393
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       O9IBD2; 23-386
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NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
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                                                                                               Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSGRPRITISFAESCKPVPQPSAFGSMKVSRDKDGSKVITVVAIPGQGPDRPQEVSYIDIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 EKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLAYIHSFGICHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 DIKPQNLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 DIKPQNLLLDPDTAVLKLCDFGSAKQLVRGRPNVSYICSRYYRAPELIFGATDYTSSIDV
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                                                                                                                                                                                                                                                                                             R SMR; Q9YH60; 23-386.

R Ensembl; ENSDARGG000017803; Danio rerio.

R GO; G0:0005524; F:ATP binding; IEA.

GO; G0:0005524; F:ATP binding; IEA.

GO; G0:000166; F:nucleotide binding; IEA.

GO; G0:0016740; F:transferase activity; IEA.

R GO; G0:0016740; F:transferase activity; IEA.

R GO; G0:0016740; F:transferase activity; IEA.

R GO; G0:0016740; F:transferase activity; IEA.

InterPro; IPR00129; Prot Linase.

R InterPro; IPR001290; Ser_thr_pkinase.

R InterPro; IPR001290; Ser_thr_pkinase.

R Pfam; PF000069; Prinase; I.

R Probom; PR00120; FRC: I.

R PROSITE; PS0010; PROTEIN KINASE DOM; I.

R PROSITE; PS0010; PROTEIN KINASE DOM; I.

R PROSITE; PS0010; RACTEIN KINASE; DAM; I.
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Mecn. Dev. 91:387-391(2000).
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family
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94.1%; Score 1959; DB 2;
Best Local Similarity 96.9%; Pred. No. 6.7e-144;
Matches 371; Conservative 7; Mismatches 5;
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NUCLEOTIDE SEQUENCE
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MEDLINE=2288257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Malaster R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Halah F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Richards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Retteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
MEDILINE-SES217008; PubMed=7720580;
Pierce S.B., Kimelman D.;
"Regulation of Spemann organizer formation by the intracellular kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L38492; AAC42224.1; -; mRNA.

R EMBL; BC108581; AA108582.1; -; mRNA.

FIR 151425; 151425.

R HSSP; P49841; 1109.

R G0; G0:0005524; F:ATP binding; IEA.

G0; G0:000166; F:nuclectide binding; IEA.

G0; G0:0004674; F:protein serine/threonine kinase activity; IEA.

G0; G0:0004674; F:protein serine/threonine kinase activity; IEA.

G0; G0:0006468; F:nuclectide binding; IEA.

G0; G0:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR000719; Proc_kinase.

R InterPro; IPR008271; Ser_thr_pkinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR00245; Tyr_pkinase.

R Pfem; PF00069; Pkinase: 1.
Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg.R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein S., Gerhard D.S.;
Submitted (NOV-2005) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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SMART; SM00220; S_TKc; 1.
                                                                                                                                                                                                                                                                                                                    Development 121:755-765(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dev. Dyn. 225:384-391 (2002)
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61 VIGNGSFGVVYQAKLCDTGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 WSAGCVLAELLIGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFFQIKAHP 300
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                                                                                                                                                                                                                                                                                                                                                                                   1 MSGRPRITSFAESCKPVQQPSSFGSMKVSRDKDGSKVIIVVATPGQGPDRQQEVIYIDTK
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95396823; PubMed=7667318;
Dominguez I., Itoh K., Sokol S.Y.;
Iroh K., Sokol S.Y.;
Iroh Gjyrogen synthase kinase 3 beta as a negative regulator dorsoventral axis formation in Xenopus embryos.";
Proc. Natl. Acad. Sci. U.S.A. 92:8498-8502(1995).
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMR; Q91627; 23-386.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0000166; F:nucleotide binding; IEA.
GO; GO:00004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                      Length 420;
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                        Serine/threonine-protein kinase; Transferase.
SEQUENCE 420 AA; 46903 MW; C02280BBBA35785D CRC64;
                                                                                                                                                                                                                  92.8%; Score 1931; DB 2; 95.3%; Pred. No. 1e-141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996, integrated into UniProtKB/TrEMBL
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                                                                                                                                                                                                                                                                                  Conservative 11; Mismatches
PROSITE; PS00107; PROTEIN KINASE ATP; 1. PROSITE; PS50011, PROTEIN KINASE DOM; 1. PROSITE; PS00108; PROTEIN KINASE ST; 1. ATP-binding; Kinase; Nucleotide-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-FEB-2006, entry version 34.
Glycogen synthase kinase 3 beta.
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 NFTTQELSSNPPLATILIPPHAR 393
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PIR; 151692, 151692.
HSSP; P49841; 1109.
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122 LRYFFYSSGEK------
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                                                                                                                                                                                                     Nature 431:946-957 (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLAYIHSFGICHR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIKPONLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQIKAHP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WSAGCVLABLLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQIKAHP 300
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PubMed=15496914; DOI=10 1038/nature03025;
Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B. Dasllva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Ectinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetradontoidea, Tetraodontidae, Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 420;
               InterPro; IPRO0011; Proc kinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001040; Prot Kinase; I.
IPR051TE; PS50011; PR0TEIN KINASE ATP; I.
IPR051TE; PS500104; PR0TEIN KINASE ST; I.
IPR051TE; PS00104; PR051TE; PR051TE
P.protein amino acid phosphorylation; IBA
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07-FEB-2006, entry version 6.
Chromosome 2 SCAF14781, whole genome shotgun sequence.
ORFNames=GSTENG00026022001;
                                                                                                                                                                                                                                                                                                                                                                                                                                          92.4%; Score 1923; DB 2;
95.0%; Pred. No. 4.2e-141;
iive 10; Mismatches 9;
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Q4S0HO;
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nes 364; Conservative
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241 PETVYRVARHYSRAKOTLPMYVKLYMYQLFRSLAYIHSPGICHRDIKPQNLLLDPETAV 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary data.

-!- FUNCTION: Plays a key role in the control of the eukaryotic cell cycle. It is required in higher cells for entry into 5-phase and mitosis. Component of the kinase complex that phosphorylates the repetitive C-terminus of RNA polymerase II. Catalytic component of MPP (By similarity).

-!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in mature oocytes (By similarity).

-!- SUBINITY: Belongs to the Ser/Thr protein kinase family.
Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||||||||||||
| LRYFFYSSGDKPDRRANRPSSVVNSMVTVGELSQWLRCKPCSQLTRARVAQAGGSQEPIR
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R GO; GO: 0005524; F.ATP binding; IEA.

R GO; GO: 000166; F:nucleotide binding; IEA.

R GO; GO: 000166; F:nucleotide binding; IEA.

R GO; GO: 0006464; F:protein serine(threonine kinase activity; IEA.

R GO; GO: 0006468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR00121; Prot kinase.

R InterPro; IPR001245; Prot kinase.

R InterPro; IPR001245; Tyr pkinase.

R InterPro; IPR001245; Tyr pkinase.

R ProDom; P0000001; Prot Kinase; 2.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00108; PROTEIN KINASE ST; 1.

R ATP-binding; Kinase; Nucleotide-binding;
                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope; Whitehead Institute Centre for Genome Research; submitted (FBS-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 496;
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SEQUENCE 496 AA; 55961 MW; 4C86362BD3301390 CRC64;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.107; Bat N.K.,

MAN Schulus R.P., Jordan H., Moore T., Manna J., Carainci P., Prange C.,

MEDLINE=22388257; Morley M.C., Hale S., Garrinci P., Prange C.,

MEDLINE=22388257; Morley M.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

MILLION D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Milling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Medriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Muthrifield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

MEDLINE=22388257; PubMed
M. Schein J.B., Jones B.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                          375
                                                                                                   301 LKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDVWSAGCVLAELLLGQP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                    316 RPRTPPEAIALCSRLLEYTPTARLTPLEACAHSFFDELRDPNVKHPNGRDTPALFNFTTQ
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20171069; PubMed=10704871; DOI=10.1016/S0925-4773(99)00300-7; Tsai J.N., Lee C.H., Jeng H., Chi W.K., Chang W.C.; Inferential expression of glycogen synthase kinase 3 genes during zebrafish embryogenesis.";
                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.

    -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH MGC Project;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                     01-MAY-1999, integrated into UniProtKB/TrEMBL. 01-MAY-1999, sequence version 1. 07-FBB-2006, entry version 38. Glycogen synthase kinase 3 alpha.
                                                                                                                                                                                           440 AA.
                                                                                                                                                                                                                                                                             Name=gskla; Synonyms=GSK3;
Brachydanio rerio (Zebrafish) (Danio rerio)
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EMBL; BC056332; AAH56332.1; -; mRNA.
                                                                                                                                                                                        PRT;
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Submitted (AUG-2003) to the
                                                                                                                                                                                        Q9YH61_BRARE PRELIMINARY;
Q9YH61;
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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE
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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE
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60 -DSGKVTTVVATPGQGPDRPQEVSYTDIKVIGNGSFGVVYQARLIDSQEMVAIKKVLQDK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 RFKNRELQIMRKLDHCNIVRLRYFFYSSGEKKDEVYLNLVLDFVPETVYRVARHFNKSKT 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 VLGTPTREQIREMNPNYTEFKFPQIRAHPWTKVFKPRTPPEAISLCSRLLEYTPVTRLSP 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 VLGTPTREQIREMNPNYTEFKFPQIKAHPWTKVFRPRTPPEAIALCSRLLEYTPTARLTP 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 TIPIIYVKVYMYQLPRSLAYIHSQGVCHRDIKPQNLLVDPDTAVLKLCDFGSAKQLVRGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNVSYICSRYYRAPELIFGATDYTSSIDVWSAGCVLAELLLGQPIFPGDSGVDQLVEIIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 KDGSKVTTVVATPGQGPDRPQEVSYTDTKVIGNGSFGVVYQAKLCDSGELVAIKKVLQDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 RFKNRELQIMRKLDHCNIVRLRYFFYSSGEKKDEVYLNLVLDYVPETVYRVARHYSRAKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 SGRPRISSFAE---PPGVPGAAAAAASAVAGGSSSGKTGGAQASGGSSSGFGNLKLGR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                           Exempli Natural Control Contro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342 LEACAHSPFDELRDPNVKHPNGRDTPALFNFTTQELSSNPPLATILIPPHAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440 AA; 48065 MW; 66A8E8D070ACA093 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.9%; Score 1704.5; DB 2; 79.1%; Pred. No. 4.7e-124; ive 26; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 SGRPRITSFAESCKPVQQP--------
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                                                                                                                                     Ensembl; ENSDARG00000015681; Danio rerio.
EMBL; BC065952; AAH65952.1; -; mRNA.
HSSP; P49841; 1Q3W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycogen synthase kinase 3 alpha.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
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NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=gsk3a;
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091BD3 BRA
10 091BD
AC 091BD
DT 01-0C
DT 01-0C
DT 07-FE
DE Glycc
GN Brach
OC Bukax
OC Actif
COC Cypri
OX NCEL
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41 29 101

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLPVIYVKLYMYQLFRSLAYIHSFGICHRDIKPQNLLLDPDTAVLKLCDFGSAKQLVRGE 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SAFGSMKVSRD 41
                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
        Shimizu T., Yamanaka Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T., Bae Y.-K., Hibi M., Hirano T., "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the formation of the dorsal organizer in zebrafish."; Mech. 91:293-303(2000).

-I. SIMILARITY: Belongs to the Ser/Thr protein kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 KDGSKVTTVVATPGQGPDRPQEVSYTDTKVIGNGSFGVVYQAKLCDSGELVAIKKVLQDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 VLGPXTREQIREMNPWYTEFKFPQIKAHPWTKVFKPRTPPEAISLCSRLLEYTPVTRLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20171051; PubMed=10704853; DOI=10.1016/S0925-4773(99)00319-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                         REMBL; AB032264; BAA22441.1; -; mRNA.

R SMR; Q91BD3; S2-412.

R Ensembl; BNSDAG0000015681; Danio rerio.

R GF, G91BD3; S2-412.

R GO; G0:0005524; F:ATP binding; IEA.

GO; G0:000166; F:muclectide binding; IEA.

GO; G0:0004674; F:protein serine/threonine kinase activity; IEA.

GO; G0:0004674; F:protein serine/threonine kinase activity; IEA.

GO; G0:0004674; F:protein amino acid phosphorylation; IEA.

R GO; G0:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR000719; Prot kinase.

R InterPro; IPR001245; Tyr_kinase.

R InterPro; IPR001245; Tyr_kinase.

R Prodom; P000001; Prot kinase; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00107; PROTEIN KINASE ST; 1.

R ATP-binding; Kinase; Nucleotide-binding;
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                                                                                                                                                                                                                                                                                                                                                                               Serine/threonine-protein kinase; Transferase.
SEQUENCE 435 AA; 47791 MW; ED77993A03D8C706 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                                                                                                                                80.2%; Score 1669.5; DB 2 78.2%; Pred. No. 2.4e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                        26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGRPRITSFAESCKPVQQP-----
                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 78.2% Matches 322; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           435 AA;
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QDNL43 CIOIN PRELIMINARY; PRT; 407 AA. Q9NL43; 01-0CT-2000, integrated into UniProtKB/TrEMBL.

CIOIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 VIGNGSFGVVYQARLIESNEMVAIKKVLQDKRFKORRELQIMRKLDHCNIVRLRYFFYSSG 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 MSGRPRITSFAESCKPVQQPSAFGSMKVSRDKDGSKVTTVVATPGQGPDRPQEVSYTDIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ensembl; ENSCINGO00001821; Clona intestinalis.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:000166; F:nuclectide binding; IEA.

R GO; GO:000166; F:nuclectide binding; IEA.

R GO; GO:00016740; F:transferase activity; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR001245; Ftr Lip pkinase.

R InterPro; IPR001245; Tyr Dkinase.

R PROSITE; PS00107; PROTEIN KINASE ATP; I.

R PROSITE; PS00107; PROTEIN KINASE DOM; I.

R PROSITE; PS00107; ROTEIN KINASE DOM; I.

R PROSITE; PS50011; ROTEIN KINASE DOM; I.

M ATP-binding; Kinase; Nucleotide-binding;

M Serine/threonine-protein kinase; Transferase.

O SEQUENCE 407 AA; 45566 MW; E71594A9B6B59F10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                molecule genes
                                                                                                                         Bukaryota, Metazoa, Chordata, Urochordata, Ascidiacea, Enterogona,
Phlebobranchia, Cionidae, Ciona.
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                                                                                                                                                                                                                                                                                        Imai K., Takada N., Satoh N., Satou Y.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for functional genomic studies in Ciona intestinalis.";
Dev. Genes Evol. 215:580-596(2005).
                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=16252120; DOI=10.1007/800427-005-0016-9; Satou Y., Satoh N.; "Cataloging transcription factor and major signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.1%; Score 1666.5; DB 283.0%; Pred. No. 3.8e-121;
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21-FEB-2006, entry version 32. Glycogen synthase kinase alpha/beta. Name-CiGSK, Synonyms-Ci-GSK alpha/beta; Ciona intestinalis.
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EMBL; AB211133; BAE06824.1; -; mRNA.
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Matches 318; Conservative
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Q9NL43; 9-368
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                                                                                                                                                                                                            Lytechinus variegatus (Sea urchin).
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Temnopleuroida, Toxopneustidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R GO; GO: 0005524; F:ATP binding; IEA.

R GO; GO: 0005524; F:ATP binding; IEA.

R GO; GO: 000566; F:nucleotide binding; IEA.

R GO; GO: 0006467; F:protein serine/threonine kinase activity; IEA.

R GO; GO: 0006468; P:protein amino acid phosphorylation; IEA.

R GO; GO: 0006468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR000271; Ser thr pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R ProDom; P0000001; Prot kinase; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00107; PROTEIN KINASE ST; 1.

R PROSITE; PS00108; PROTEIN KINASE ST; 1.
                                                                                                                                                                                                                                                                                                                        Pubmed=15151983; DOI=10.1242/dev.01152; Weitzel H.E., Illies M.R., Byrum C.A., Xu R., Wikramanayake A.H., Ettensohn C.A.; Byrum C.A., Tollies M.R., Byrum C.A., Tollies M.R., Byrum C.A., Tollies M.R., Byrum C.A., Tollies M.R., Botallity of {beta}-catenin along the animal-vegetal axis of the sea urchin embryo mediated by dishevelled."; Development 131:2947-2956(2004).
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
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SEQUENCE 414 AA; 46202 MW; 276988692DF90815 CRC64;
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80.5%; Pred. No. 1.9e-118;
tive 35; Mismatches 37;
                                                                                             QĞIUGS_LYTVA PRELIMINARY; PRT; 414 AA. Q6IUGS_LOGY, integrated into UniProtKB/TrEMBL. 05-JUL-2004, sequence version 1. 07-FBB-2006, entry version 14. Glycogen synthase kinase-3.
346 NFTDKELSIKSPLNNILIPLHAR 368
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HSSP; P24941; 1AQ1.
SMR; Q6IUG5; 23-381.
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Best Local Similarity 80.5%
Matches 306; Conservative
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        Db
        242 SAGCVLAELLIGQPIPPGDSGVDQLVBIIKVLGTPSRDQIKEMNPNTTERKFPQIKEHPW 301

        Cy
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        Cy
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        Cy
        372 FTTGBLSSNPPLATILIPPH 391

        Db
        362 FTAGELSKPSIRTALIPPH 381
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Search completed: September 15, 2006, 17:12:10 Job time: 306 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on:

September 15, 2006, 17:03:15; Search time 195 Seconds (without alignments) 923.812 Million cell updates/sec

US-10-733-816-2

Perfect score:

2081 1 MEYMPWEGGGMSGRPRTTSF.....QELSSNPPLATILIPPHARI 394 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2589679 seqs, 457216429 residues Searched:

Total number of hits satisfying chosen parameters:

2589679

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_8:* Database

geneseqp2000s:* geneseqp2001s:* geneseqp2001s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:*

SUMMARIES

No. Score Match Length DB ID Description 1 2081 100.0 394 5 ABB07578 2 2024 97.3 420 4 ABB07578 4 2024 97.3 420 7 ABB144294 5 2024 97.3 420 7 ABB144294 8 2024 97.3 420 8 AAB805377 7 2024 97.3 420 8 AAB80537 8 2024 97.3 420 8 AAB80537 9 2024 97.3 420 8 AAB80537 10 2013 96.7 420 8 AAB80537 11 2013 96.7 420 8 AAB80538 12 2013 96.7 420 8 AAB80537 13 2013 96.7 420 5 AAB817875 14 2013 96.7 420 5 AAB870714 15 2013 96.7 420 6 AAB870714 16 2013 96.7 420 6 AAB870714 17 2013 96.7 420 7 AAB844293 18 2013 96.7 420 7 AAB844293 19 2013 96.7 420 7 AAB844293 10 2013 96.7 420 7 AAB844293 11 2013 96.7 420 8 AAB80320 12 2013 96.7 420 8 AAB80320 13 2013 96.7 420 7 AAB844293 14 2013 96.7 420 8 AAB80320 18 2013 96.7 420 8 AAB80320 20 2013 96.7 420 8 AAB80320 20 2013 96.7 420 8 AAB80320 21 2013 96.7 420 8 AAB80320 22 2013 96.7 420 9 AAB839562 22 2013 96.7 420 9 AAB839564 22 2013 96.7 420 9 AAB839564 22 2013 96.7 420 9 AAB839564 23 2013 96.7 420 9 AAB839564 24 AAB839564		de			COLUMNIA	
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96.7 420 9 AEA39564 Aea39564 96.7 420 9 AEB28124 Aeb28124	2013	96.7	420	σ	AEA39562	Aea39562 Human gly
96.7 420 9 AEB28124 Aeb28124	2013	96.7	420	9	AEA39564	Aea39564 Mouse gly
	2013	96.7	420	6	AEB28124	Aeb28124 Human gly

Aec81932 Human gly	Aee06398 Glycogen	Adc50594 Human tau	Aar61326 Tau-prote	Abr82106 Human gly	Abr44289 Human gly	Ade64051 Rat Prote	_	Abr44295 Human gly	Abr44298 Human gly	Human	Human	Ado49107 Human ded	Adu20919 Human gly	Adu06409 Novel bro	Aeb25735 Human and	Aec34201 Human GSK	Aee06396 Glycogen	Adre6057 Human pro	Adr66399 Human pro	Ady85481 Catalytic	Aee06402 Glycogen
AEC81932	AEE06398	ADC50594	AAR61326	ABR82106	ABR44289	ADE64051	ADI28893	ABR44295	ABR44298	ADJ69554	ADH09633	ADO49107	ADU20919	ADU06409	AEB25735	AEC34201	AEE06396	ADR66057	ADR66399	ADY85481	AEE06402
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420	420	428	420	420	420	420	420	433	433	433	433	433	433	433	433	433	433	439	439	385	387
7.96	96.7	7.96	9.96	9.96	9.96	9.96	96.6	95.9	95.9	95.9	95.9	95.9	95.9	95.9	95.9	95.9	95.9	95.9	95.8	95.1	92.2
2013	2013	2013	2010	2010	2010	2010	2010	1996.5	1996.5	1996.5	1996.5	1996.5	1996.5	1996.5	1996.5	1996.5	1996.5	1996.5	1994.5	1978	1919
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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GSK3; glycogen synthase kinase 3; GSK3alpha; GSK3beta; nootropic; human; Alzheimer's disease; antiinflammatory; antidiabetic; gene therapy.
                                                                                                   1. .10
/note= "Glu-tag and Gly linker"

    .394
    /note= "truncated GSK3beta"

                                                 Human truncated GSK3beta polypeptide 557.
                                                                                            Location/Qualifiers
             ABB07578 standard; protein; 394 AA
                                     08-MAY-2002 (first entry)
                                                                                 Ното варіепв
                         ABB07578;
                                                                                                  Peptide
                                                                                                              Peptide
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WO200210357-A2.

25-JUL-2001; 2001WO-US023539. 07-FEB-2002.

(CHIR) CHIRON CORP.

27-JUL-2000; 2000US-0221242P.

Fang EY; SD, Hall JA, Calderon-Cacia M, Zhong Z, Nguyen SH, Medina-Selby A; Harrison SD, Hall JA, Coit DG,

WPI; 2002-188732/24.

New glycogen synthase kinase 3 (GSK3) inhibitors and nucleic acids encoding them, useful for treating diseases mediated by GSK3 activity, including Alzheimer's disease, type 2 diabetes and inflammation.

Claim 8; Fig 2A-B; 36pp; English.

The invention provides glycogen synthase kinase 3 (GSK3) polypeptides capable of crystallisation, including GSK3alpha and GSK3beta polypeptides. The GSK polypeptides can be used to identify and optimise GSK3 inhibitors. Nucleic acid encoding the GSK polypeptides are useful as

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DIKPONLLLDPDTAVLKLCDFGSAKOLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibiting expression of glycogen synthase kinase 3 beta in cells and for diagnosing, treating neurological and insulin regulation disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG 120
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                                                                         The invention relates to antisense compounds targetted to nucleic acid encoding glycogen synthase kinase 3-beta (GSK3B) (also known as tau protein kinase I (TPK-1). The antisense compound is useful for inhibiting the expression of glycogen synthase kinase 3-beta enzyme in cells or tissues and for treating diseases or conditions associated with the enzyme such as insulin regulation disorder, in particular diabetes and neurological disorder, e.g. Alzheimer's disease and bipolar illness. The antisense compound is also useful for diagnosing diseases associated with the expression of glycogen synthase kinase 3-beta and for prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation and as a research reagent. The present sequence is human glycogen synthase kinase 3-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glycogen synthase kinase 3; GSK3alpha; GSK3beta; nootropic; human;
imer's disease; antiinflammatory; antidiabetic; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                              11 MSGRPRITSFAESCKPVQQPSAFGSMKVSRDKDGSKVTTVVATPGQGPDRPQEVSYTDTK
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                                                                                                                                                                                                                                                                                                                               97.3%; Score 2024; DB 4; Length 420;
100.0%; Pred. No. 5e-210;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human glycogen synthase kinase 3beta (GSK3beta) polypeptide.
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250. .419
                                                   Example 13; Page 88-90; 106pp; English
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                                                                                                                                                                                                                                                                                                  Sequence 420 AA;
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Alzheimer's
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pharmaceutical agents, for treating diseases mediated by GSK3 activity, including Alzheimer's disease, type 2 diabetes and inflammation. The present sequence represents the amino acid sequence of a truncated GSK3beta polypeptide 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel antisense compounds, particularly antisense oligonucleotides for
                                                                                                                                                                                                                                                                                                                   RLRYFFYSSGEKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLA
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                                                                                                                                                                                                               MEYMPMEGGGMSGRPRTTSFAESCKPVQQPSAFGSMKVSRDKDGSKVTTVVATPGQGPDR
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                                                                                                                   100.0%; Score 2081; DB 5; Length 394; 100.0%; Pred. No. 2.9e-216; ive 0; Mismatches 0; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wyatt JR;
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Matches 394; Conservative
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                                                                                     Sequence 394 AA;
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GSK3; angiogenesis; glycogen synthase kinase-3; antilipemic; cardiant; vulnerary; antiarteriosclerotic; GSK3beta; enzyme.

Homo sapiens

(SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC

Walsh K;

23-OCT-2002; 2002WO-US033909 29-OCT-2001; 2001US-0350160P 13-NOV-2001; 2001US-0337905P

08-MAY-2003

Human glycogen synthase kinase-3 (GSK3)beta polypeptide

(first entry)

18-AUG-2003

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standard; protein;

ABR44294 ABR44294;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides glycogen synthase kinase 3 (GSK3) polypeptides capable of crystallisation, including GSK3alpha and GSK3beta polypeptides. The GSK polypeptides can be used to identify and optimise GSK3 inhibitors. Nucleic acid encoding the GSK polypeptides are useful a pharmaceutical agents, for treating diseases mediated by GSK3 activity, including Alzheimer's disease, type 2 diabetes and inflammation. The present sequence represents the amino acid sequence of human GSK3beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New glycogen synthase kinase 3 (GSK3) inhibitors and nucleic acids encoding them, useful for treating diseases mediated by GSK3 activity, including Alzheimer's disease, type 2 diabetes and inflammation.
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                                                              /note= "specifically claimed fragment" 351. .384
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/note= "specifically claimed fragment"
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100.0%; Pred. No. 5e-210;
iive 0; Mismatches 0;
                   "specifically claimed
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                     /note= "sp
285. .384
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384; Conservative
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Coit DG, Nguyen SH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 420 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to inhibiting/enhancing angiogenesis. The method involves administering to a subject needing the treatment, an angiogenesis inhibitor/promocter, such as an active/inactive glycogen synthase kinase-3 (GSK3) molecule or a GSK3 kinase activator/inhibitor, where the angiogenesis modulator is administered to inhibit/enhance angiogenesis in a subject. The methods are useful for treating a condition associated with increased apoptotic cell death of vascular endothelial cells, where the condition is characterized by lesion of blood vessel wall, such as hyperlipidemia, also in the treatment of sequence represents a human GSK3beta polypeptide (Genbank Accession No. $53324)
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                                                                                                                                                                                                                                                                                                                                                                           modulating angiogenesis, useful for treating hyperlipidemia, comprist administering an angiogenesis inhibitor/promoter, such as an active/inactive glycogen synthase kinase-3 (GSK3) molecule or a GSK3 activator/inhibitor.
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live 0; Mismatches
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Matches 384; Conservative
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WIKVFRPRIPPEAIALCSRLLEYTPTARLTPLEACAHSPFDELRDPNVKHPNGRDTPALF 360

NFTTQELSSNPPLATILIPPHARI 394

361

RESULT

WSAGCVLAELLLGOPIFPGDSGVDQLVEIIKVLGTPTREQIREMNDNYTEFKFPQIKAHP 300 WTKVFRPRTPPEAIALCSRLLEYTPTARLTPLEACAHSFFDELRDPNVKHPNGRDTPALF 370

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel Drosophila species DNA sequences and their encoded proteins with their corresponding human homologues. The proteins or their encoding polynuclectides are useful in a method of prevention, treatment or diagnosis of a disease in an individual, and used to identify a substance capable of binding to the polypeptide or modulating the polypeptide or modulating the polypeptide or modulating the polypeptide. The function of the polypeptide comprisising inclubating the polypeptide of the polypeptide. The compositions are administered to an individual in the polypeptide. The compositions are administered to an individual in the polypeptide. The apply and a biological sample comprising the mucleic acid such as DNA or the polymucleotide is detected in a biological sample, comprises brining the biological sample containing the nucleic acid such as DNA or than incontact with a probe comprising a fragment of at least 15 and electing any duplex formed between the probe and nucleic acid in the sample. The method also comprises providing an antibody capable of binding to the polypeptide, incubating a biological sample with the antibody to allow the formation of an antibody-antigen complex, and determining whether antibody-antigen complex and account and isease such as cancer. The antibody or identified substance is also useful in inhibiting the function of a polypeptide
                                                                          241 WSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQIKAHP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Drosophila polypeptides and polynucleotides, useful for diagnosing, preventing and/or treating disorders, such as cancer, glomerulonephritis, rheumatoid arthritis, psoriasis, malaria, emphysema and alopecia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; cardiovascular; immunosuppressive; nephrotropic; antirheumatic; antiarthritic; dermatological; antipsoriatic; antiinflammatory; fungicide; gene therapy; Drosophila; diagnosis; cardiovascular disorder; autoimmune disease; glomerulonephritis; rheumatoid arthritis; dermatological disorder; psoriasis; inflammatory disorder; malaria; emphysema; alopecia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human glycogen synthase kinase 3 beta protein.
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                                                                                                                                                  NFTTQELSSNPPLATILIPPHARI 394
                                                                                                                                                                              3xample 27; Page 218; 265pp; English
                                                                                                                                                                                                                                                                                                                         ADK11467 standard; protein; 420 AA
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27-NOV-2001; 2001GB-00028384.
11-FEB-2002; 2002GB-00003185.
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                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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and/or regulating a cell division cycle function. The diseases also include cardiovascular disorders, autoimmune diseases such as glomerulonephritis and rheumatoid arthritis, and dermatological disorders such as psoriasis, inflammatory, fungal, and parasitic disorders such as malaria, emphysema and alopecia. This sequence represents a human homolg for one of the Drosophila proteins of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG
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                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Matches 384; Conservative
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                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                 Sequence 420 AA;
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The invention relates to a novel method for identifying an antiviral compound. The novel method comprises exposing a cell that expresses a host factor to a candidate compound to identify an agent that inhibits the expression or activity of the host factor. The novel method involves identifying an antiviral compound, comprising exposing a first cell that expression or activity of the host factor in the first cell, where a candidate compound that inhibits the expression or activity of the host factor in the first cell, where a candidate compound that inhibits the compound and a retrovirus, and determining whether the compound inhibits the ability of the retrovirus to infect or replicate within the second cell, where a potential antiviral compound. The method is useful in identifying antiviral agents, including the ability of the retrovirus to infect or replicate within the second cell, where a potential antiviral compound that inhibits the ability of the retrovirus to infect or compound. The method is useful in identifying antiviral agents, including those that are effective against retroviruses, such as HIV. This sequence represents a human host factor protein used in the antiviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSG 120
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100.0%; Pred. No. 5e-210;
ive 0; Mismatches 0; Indels
                                       Claim 13; SEQ ID NO 165; 141pp; English
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Best Local Similarity 100.
Matches 384; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 420 AA;
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The invention relates to a novel method for identifying a compound capable of treating a hematological disorder which comprises combining a compound to be tested with a specific polypeptide under conditions as suitable for binding of the test compound to the polypeptide. The method of the invention has haematological and cytostatic applications and may be useful for identifying compounds for treating a haematological disorder associated with erythroid cells e.g. anaemia and erythrocytosis, bone marrow e.g. leukaemia, platelets e.g. thrombocytopenia and transpass or Ba-cells and T-cells e.g. neutropenia. The compounds identified may be utilised during gene therapy procedures. The current sequence is that of a human haematological disorder-related protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying a compound capable of treating a hematological disorder comprises combining a compound to be tested with a polypeptide related with the disorder under conditions suitable for binding of the test compound to the polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                    Healy A;
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2003US-0502909P.
2003US-0510351P.
2003US-0512380P.
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2003US-0456320P.
2003US-0460279P.
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2003US-0470052P
2003US-0498106P
                                                                                                    05-FEB-2004; 2004WO-US003417
                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                      2004-625850/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADR40190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 420 AA;
                                  WO2004072242-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention.
   Homo sapiens.
                                                                                                                                                       18-FEB-2003;
                                                                                                                                                                       20-MAR-2003;
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                                                                                                                                                                                                          28-APR-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a method of identifying a candidate branching morphogenesis modulating (MBM) agent. The method comprises: providing an assay system comprising a MBM polypetide or nucleic acid; contacting the assay system modulating and the presence of the system provides a reference activity, except for the presence of the test agent; and detecting a test agent-blased activity of the assay system, where a difference between the test agent-blased activity and the reference activity identifies the test agent as a candidate branching morphogenesis in a mammalian cell; and a method of modulating morphogenesis in a mammalian cell; and a method for diagnosing a disease in a patient. The method is useful in identifying a candidate branching morphogenesis modulating agent for preparing a composition for diagnosing or treating cancer. This is the amino acid sequence of a human branching morphogenesis modulating (MBM) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying a candidate branching morphogenesis modulating agent for treating cancer comprises contacting the assay system comprising a MBM polypeptide or nucleic acid with a test agent and detecting a test agent-biased activity.
                WIKVFRPRITPPEALALCSRILEYTPTARLTPLEACAHSPFDELRDPNVKHPNGRDTPALF 360
WTKVFRPRTPPEAIALCSRLLEYTPTARLTPLEACAHSFFDBLRDPNVKHPNGRDTPALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Karim FD, Swimmer C, Habeck HA, Koblizek II;
r S, Langheintich U, Stott GM, Trowe T, Vogel AM;
Scheel JK, Mill TT, Jin Y, Bjerke LM, Hai B;
, Lickteig K, Hammonds RGR, Amundsen CD, Zhang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 420;
                                                                                                                                                                                                                                                                                           cytostatic; gene therapy; human;
branching morphogenesis modulating agent; MBM agent.
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100.0%; Pred. No. 5e-210;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3, SEQ ID NO 36; 179pp; English.
                                                           NFTTQELSSNPPLATILIPPHARI 394
                                                                               ADS92965 standard; protein; 420 AA
                                                                                                                                                                                                                                                                Glycogen synthase kinase 3 beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002US-0420554P.
2002US-0436941P.
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                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EXEL-) EXELIXIS INC.
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Adamkewicz JI,
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30-DEC-2002;
                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                    ADS92965;
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Neuroregenerative drug for treating neurological disease e.g. Parkinson's disease, Alzheimer's disease and Down's syndrome, contains substance which inhibits activity of glycogen synthase kinase-3 as active
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neuroregenerative drug; glycogen synthase kinase-1; GSK-3; neurological disease; Parkinson's disease; Alzheimer's disease; bown's syndrome; cerebrovascular accident; stroke; spinal injury; Huntington's chorea; multiple sclerosis; amyotrophic lateral sclerosis; epilepsy; anxiety disorder; schizophrenia; depression;
                                                                                                                                               121 EKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLAYIHSFGICHR
                                                                        61 VIGNGSPGVVYQAKLCDSGELVAIKKVLQDKRPKNRELQIMRKLDHCNIVRLRYFFYSSG
                                                                                                                                                                                                            71 VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG
                                                                                                                        EKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLAYIHSFGICHR
                                                                                                                                                                                          DIKPONLLLDPDTAVLKICDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human glycogen synthase kinase-3-related protein - SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                   371 NFTTOELSSNPPLATILIPPHARI 394
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Conservative

Similarity

Best Local Simi Matches 384;

Query Match

11 MSGRPRITSFAESCKPVQQPSAFGSMKVSRDKDGSKVTTVVATPGQGPDRPQEVSYTDTK 70

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AAR61327;
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                                                                                                                                                                                                                        DIKPQNLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 250
                                                                                                                                                                                                                                   DIKPQNLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 240
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                                                                                                                                                                                                                                                                         WSAGCVLAELLIGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQIKAHP 300
                                                                                                                                                                                                                                                                                                              WIKVERPRIPPEAIALCSRILEYIPIARLIPLEACAHSFPELRDPNVKHPNGRDIPALF 360
                                                                                                                                                                                   EKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLAYIHSFGICHR 190
                                                                                                                                                                                                                                                                                                   WTKVFRPRTPPEAIALCSRLLEYTPTARLTPLEACAHSFFDELRDPNVKHPNGRDTPALF 370
    anxiety
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cerebrovascular accident, stroke, spinal injury, Huntington's chorea, multiple sclerosis, amyotrophic lateral sclerosis, epplopsy, anxiety disorder, schizophrenia, depression and manic-depressive psychosis. Th present human protein is used in the exemplification of the invention.
                                                                                                                        1 MSGRPRITSFAESCKPVQQPSAFGSMKVSRDKDGSKVTTVVATPGQGPDRPQEVSYTDTK
                                                                                                                                            VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG
                                                                                                       MSGRPRTTSFAESCKPVOOPSAFGSMKVSRDKDGSKVTTVVATPGOGPDRPOEVSYTDTK
                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Switch control ligand; switch control pocket; protein activity modulation; human; p38-alpha kinase; enzyme.
                                                                 Length 420;
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                                                                Score 2024; DB 8;
Pred. No. 5e-210;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                            384
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100.0%; Pred
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31-DEC-2002; 2002US-0437403P.
31-DEC-2002; 2002US-0437415P.
31-DEC-2002; 2002US-0437487P.
18-APR-2003; 2003US-0463804P.
24-DEC-2003; 53US-00463804.
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                                                                                    Conservative
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                                              Sequence 420
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                                                                                   384;
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                                                                Query Match
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which interact with proteins e.g. enzymes, receptors, or signaling, which interact with proteins e.g. enzymes, receptors, or signaling proteins, in order to regulate the activity of the proteins. The method comprises identifying a switch control ligand forming a part of the protein; identifying a switch control ligand forming a part of the protein and which interacts with the switch control ligand, where the ligand interacting in vivo with the pocket to regulate the conformation and biological activity of the protein so that the protein will assume a first conformation and a first biological activity upon the ligand-pocket interaction, and will assume a second different conformation and a biological activity in the absence of the ligand-pocket interaction, providing respective samples of the protein in the first and second conformations, and screening at least one of the samples against one or more candidate molecules by contacting the molecules and one sample, identifying small molecules which bind with the protein at the region of the both for modulating protein activity of the protein. The meethod is useful for modulating protein activity of the identification of new pharmacological compounds and for treatment modalities. The present conforms is ableased to which a switch control ligand was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190
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Identifying molecules that interact with specific naturally occurring proteins for modulating protein activity, comprises identifying molecules that bind with the protein at the region of the pocket to regulate
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                                                                                                                                                                                                                                                 invention relates to a method for identifying molecules
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Pred. No. 7.6e-209;
0; Mismatches 1;
                                                                                                                                                                             SEQ ID NO 31; 204pp; English.
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Best Local Similarity 99.7%;
Matches 383; Conservative C
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(first entry)
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21-APR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ67459 codes for a newly isolated tau-protein kinase I enzyme (TPK-1), shown in AAR61327 (compare to human AAR61326). The cDNA was cloned from a art fetuse brain cDNA library, and was expressed in insect cells. TPK-I acts specifically on tau-protein, which is thought to be involved in Alzhaimer's disease (AD) and senile dementia of the AD type. It is hoped that the characterisation of TPK-I may lead to development of new agents for the prevention and therapy of these diseases. (Updated on 25-WAR-2003 to correct PA field.) (Updated on 25-WAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQIKAHP 310
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                                                                                                                                                                                                                                                                                                                                          Newly isolated tau-protein kinase I enzyme - with specificity for protein providing means for prevention and treatment of Alzheimer'
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                                                                                                                                                                                                                                                            Shiratsuchi
                          Tau-protein kinase I enzyme; TPK-I; Alzheimer's disease.
Tau-protein kinase I (TPK-I), Alzheimer's disease
                                                                                                                                                                                                                                                            Saito K,
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                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 18; 30pp; English.
                                                                                                                                                                                                                    CORP.
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93JP-00085143.
93JP-00191246.
                                                                                                                                     94EP-00103057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 420 AA;
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02-AUG-1993;
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The specification describes the structure of glycogen synthase kinase (GSK)3beta protein in crystalline form. GSK3beta is frequently rearranged in advanced T-cell lymphomas. The crystalline structure of GSK3beta is useful in the design or selection of potential inhibitors and/or activators of GSK3beta kinase activity. Such inhibitors and activators are useful for treating Type II disbetes mellitus, obesity, neurodegenerative disorders such as Alaheimer's disease, stroke and mood disorders such as bipolar and unipolar depression, schizophrenia, cancer, in humans. Because GSK3beta may crystallize in more than one crystallic form, the structure coordinates of GSK3 or its portions are particularly useful to solve the structure of GSK3 mitants, GSK3. They may also be used to solve the structure of GSK3 mitants, GSK3 co-complexes, or of the crystalline form of any other protein, particularly kinases with significant anino acid sequence homology to any functional domain of GSK3. The present sequence represents the beta isoform of GSK3beta
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                                                                                                                                                                                                                                                                                    Glycogen synthase kinase 3 beta; GSK3beta; T-cell lymphoma; stroke; Type II diabetes mellitus; obesity; neurodegenerative disorder; cancer; Alzheimer's disease; mood disorder; depression; schizophrenia; cyclin-dependent kinase 2; substrate; protein coordinate data.
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                                                                                                                                                                                                                      Amino acid sequence of glycogen synthase kinase 3 isoform beta.
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iive 0; Mismatches 1;
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ABB77875 standard; peptide; 420
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14-AUG-2001; 2001GB-00019796.
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hes 383; Conservative
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Modulating angiogenesis, useful for treating hyperlipidemia, administering an angiogenesis inhibitor/promoter, such as an

baldness

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181 251 241 311 301 371 361

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allergy, asthma, Huntington's disease, Parkinson's disease, AIDS-related dementia, amyotrophic lateral sclerosis (Lou Gehrig's disease), multiple sclerosis, cardiomyocyte hypertrophy, reperfusion/ischaemia and baldness. The present sequence is human (SK-3 beta, used to illustrate the invention. GSK-3 beta is a serine/threonine protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSK3; angiogenesis; glycogen synthase kinase-3; antilipemic; cardiant; vulnerary; antiarteriosclerotic; GSK3beta; enzyme.
                                                                                                                                                                                                                                                                                                                              VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG
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                                                                                                                                                             Score 2013; DB 6;
Pred. No. 7.8e-209;
0; Mismatches 1;
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ilarity 99.7%;
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                                                                                                                                                                                                                                       WIKVFRPRIPPEAIALCSRLLEYTPTARLTPLEACAHSFFDELRDPNVKLPNGRDTPALF 360
    EKKDEVYLNLVLDYVPETVYRVARHYSRAKOTLPVIYVKLYMYQLFRSLAYIHSFGICHR 180
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                                                                 DIKPONLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human glycogen synthase kinase-3 beta
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27-FEB-2002; 2002US-0361899P.
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Homo

92JP-00177241

2003-460769/44

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Disclosure; Page 11-13; 29pp; Japanese.
                                                                                           Phosphorylation of tau protein
                                 (MITU ) MITSUBISHI CHEM CORP.
                                                                   N-PSDB; ADD68695
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                                                      The invention relates to inhibiting/enhancing angiogenesis. The method anglogenesis inhibitor/promoter, such as an active/inactive glycogen synthase kinase-3 (GSK3) molecule or a GSK3 kinase activator/inhibitor, where the angiogenesis modulator is administered to inhibit/enhance angiogenesis in a subject. The methods are useful for treating a condition associated with increased apoptotic cell death of vascular endothelial cells, where the condition is characterized by lesion of Mood vessel wall, such as hyperlipidem, also in the treatment of myocardial infarction and in the promotion of would healing. The present sequence represents a human GSK3beta polypeptide (GenBank Accession No.
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active/inactive glycogen synthase kinase-3 (GSK3) molecule or a GSK3 activator/inhibitor.
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                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                  Length
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Pred. No. 7.8e-209;
                                                                                                                                                                                                                                                         0; Mismatches
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                                    Disclosure, Page 97-99; 115pp; English
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The invention relates to a novel method for the phosphorylation of tau protein in which tau protein or its partial peptide is phosphorylated the action of phosphoenzyme I, a serine-threonine phosphorylase. The method of the invention may be used for elucidation of the cause of Alzheimer's disease and Alzheimer type senile dementia. The current sequence is that of the rat tau phosphorylation-related protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG
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                                                                                                                                                                                                                                        Score 2013; DB 7;
Pred. No. 7.8e-209;
0; Mismatches 1;
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He : 199 secs
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                                                                                                                                                                                                                                           96.7%;
                                                                                                                                                                                                                                                                 Best Local Similarity 99.7
Matches 383, Conservative
                                                                                                                                                                                              Sequence 420 AA;
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

September 15, 2006, 17:07:20 ; Search time 40 Seconds (without alignments) 947.735 Million cell updates/sec Run on:

Title: Perfect score:

US-10-733-816-2 2081 1 MEYMPWEGGGMSGRPRTTSF.....QELSSNPPLATILIPPHARI 394 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	glycogen synthase	tau-protein kinase	intracellular kina	õ	protein kinase (EC	protein kinase sgg	probable protein k	protein kinase sgg	~		protein			serine/threonine-s	protein kinase MSK	probable shaggy-li	shaggy protein kin	shaggy protein kin	protein kinase ASK	shaggy-like protei	protein kinase MSK	tau-protein kinase	shaggy-like protei	probable shaggy-li	protein kinase ASK	shaggy-like protei	probable glycogen	-⊢	hypothetical prote
SUMMARIES	ID	S53324	TVRTKB	151425	151692	TVRTKA	835327	S10932	S35423	T26520	S51105	T03601	T02297	T48637	T01236	S37642	T03777	851106	T02256	841597	871266	S37643	S52095	T04863	A84715	S41596	S77922	A96613	T02254	F86232
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de	Query Match	97.3	96.6	95.8	92.4	77.2	76.4	74.1	74.1	64.5	62.3	61.3	61.2	60.8	60.5	60.4	60.0		59.9	59.9	59.8	59.8		59.3	•	ď.	٩.	59.1	59.1	59.0
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protein kinase MSK	shaggy-like protei	protein kinase AtK	hypothetical prote	protein kinase (EC	shaggy-like kinase	protein kinase skp	protein kinase skp	serine-threonine p	probable protein k	glycogen synthase	hypothetical prote	protein kinase RIM	MRK1 protein - yea	probable serine/th	hypothetical prote
44	6	8	26	. 91	80	28	88	91	89		1	7	πi	6.	37
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1 8376	2 T0813	2 \$5193	2 T017	2 A554	2 T479	2 T377	2 T4513	2 T4074	2 T4300	2 T1845	2 F9012	2 A5634	2 \$6761	2 T0411	2 T199
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58.9 411 1	468 2	58.6 421 2	58.0 447 2 '	56.6 468 2	55.6 431 2	55.6 387 2	53.3 354 2	47.9 381 2	47.9 390 2	47.0 452 2	45.2 354 2	45.2 370 2	501 2 8	38.1 211 2 1	35.3 367 2 7

ALIGNMENTS

RESULT 1 553324 91ycogen synthase kinase 3 beta (EC 2.7.1) - human Glycocles: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: S53324 Biochem. J. 303, 701-704, 1994 A;Title: Mitogen inactivation of glycogen synthase kinase-3-beta in intact cells via ser A;Reference number: S53324; MUID:95071278; PMID:7980435 A;Accession: S53324 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Notecute Type: MINAMAA, A;Residues: 1-420 <sta> A;Residues: 1-420 <sta> A;Residues: 1-420 <sta> A;Cross-references: UNIPROT:P49841; UNIPARC:UPI000004E93D; EMBL:L33801; NID:g529236; PID: A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994 C;Comment: This enzyme is inhibited by phosphorylation of serine 9 by p70 S6 kinase (see C;Genetics: GDB:GSK3B</sta></sta></sta>
A,Cross-references: GDB:6108057 C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; phosphorotein; phosphotransferase F;54-315/Domain: protein kinase homology <kin> F;62-70/Region: protein kinase ATP-binding motif F;9/Binding site: phosphate (Ser) (covalent) (by ribosomal protein S6 kinase) #status ex F;85/Active site: Lys #status predicted</kin>

Gaps ô Query Match 97.3%; Score 2024; DB 1; Length 420; Best Local Similarity 100.0%; Pred. No. 2.6e-89; Matches 384; Conservative 0; Mismatches 0; Indels 0

Matches Qy	38,	Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps (1 MSGRPRTTSFAESCKPVQQPSAFGSMKVSRDKDGSKVTTVVATPGQGPDRPQEVSYTDTK 70 1 MSGRPRTTSFAESCKPVQQPSAFGSMKVSRDKDGSKVTTVVATPGQGPDRPQEVSYTDTK 60	0,70
ò	71	71 VIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSG 130	130
qq	61		120
οy	131	EKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVI YVKLYMYQLFRSLAYTHSFGI CHR	190
Db	121		180
δ	191	DIKPONLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 250	250
Db	181		240
ογ	251	WSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQIKAHP 310	310
qa	241		300

311 WIKVFRPRIPPEALALCSRLLEYTPTARLTPLEACAHSFFDELRDPNVKHPNGRDTPALF 370

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CyAccession: 151425
R;Pierce, S.B.; Kimelman, D.
Development 121, 755-765, 1995
A;Title: Regulation of Spemann organizer formation by the intracellular kinase Xgsk-3.
A;Title: Regulation of Spemann organizer formation by the intracellular kinase Xgsk-3.
A;Title: Regulation of Spemann organizer formation by the intracellular kinase Xgsk-3.
A;Title: Regulation of Spemann organizer formation by the intracellular kinase Xgsk-3.
A;Reference number: 151425; MUID:95237008; PMID:7720580
A;Reference number: 151425; MUID:95237008; PMID:7720580
A;Reference rumber: 151425; MUID:97237008; PMID:9727189; PIDN:1
A;Residues: 1-420 <PIE>
A;Residues: 1-420 <PIE>
A;Genetics:
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R;Dominguez, I.; Itch, K.; Sokol, S.Y.
Proc. Natl. Acad. Sci. U.S.A. 92, 8498-8502, 1995
A;Title: Role of glycogen synthase kinase 3 beta as a negative regulator of dorsoventral A;Reference number: 151692; MUID:95396823; PMID:7667318
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                                                                                                                                                                                                                        intracellular kinase (EC 2.7.1.-) - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
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A;Molecule type: mRNA
A;Residues: 1-420 <DOM>
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Best Local Similarity 95.34
Matches 365; Conservative
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: S14708; S33741; S36729
R;Woodgett, J.R.
BENBO J. 9, 2431-2438, 1990
A;Teference number: S14708
A;Accession: S14708
A;Accessio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Article: Glycogen synthase Kinase 3-beta is identical to tau protein kinase I generating A; Reference number: S33741; MUID:93307488; PMID:7686508
A; Accession: S33741
A; Accession: S33741
A; Accession: S33741
A; Residues: 1-239, VV, 241-420 <1SH>A; Residues: 1-239, VV, 241-420 <1SH>A; Residues: In Signature and Signature a
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A;Molecule type: protein
A;Residues: 37-58;61-74;151-158;293-316;318-325;327-332;351-368;370-375 <1SH2>
A;Cross-references: UNIPARC:UP10000172536; UNIPARC:UP10000172537; UNIPARC:UP10000172538;
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MSGRPRTTSFAESCKPVQQPSAFGSMKVSRDKDGSKVTTVVATPGQGPDRPQEVSYTDTK
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96.6%; Score 2010; DB 1;

Best Local Similarity 99.5%; Pred. No. 1.2e-88;

Matches 382; Conservative 1; Mismatches 1;
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A; Molecule type: mRNA
A; Residues: 1-42 < RU3>
A; Cross-references: UNIPARC:UP1000016BD6B; EMBL:X70865; NID:g11149; PIDN:CAA50215.1; PID
A; Cross-references: UNIPARC:UP1000016BD6B; EMBL:X70865; NID:g11149; PIDN:CAA50215.1; PID
A; Siegfried, E.; Chou, T.B.; Perrimon, N.
R; Siegfried, E.; Chou, T.B.; Perrimon, N.
A; Title: wingless signaling acts through zeste-white 3, the Drosophila homolog of glycoge
A; Reference number: A44331; MUID:93113685; PMID:1335365
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rossiduse: 1-243, '1, 245-405, 'A', 407-512,'D', 514 <BOU>
A;Cross-references: UNIPARC:UP1000016BD69; EMBL:X53332; NID:g10895; PIDN:CAA37419.1; PID
R;Siegfried, E.; Perkins, L.A.; Capaci, T.M.; Perrimon, N.
Rxurrs 345, 825-829, 1990
A;Title: Putative protein kinase product of the Drosophila segment-polarity gene zeste-wh
A;Reference number: S10931; MUID:90294930; PMID:2113617
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A;Residues: 1-289 <SI2>
A;Cross-references: UNIPARC:UP1000016BE19; EMBL:X54005; NID:g8859; PIDN:CAA37951.1; PID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Title: Functional significance of a family of protein kinases encoded at the shaggy loc
A,Reference number: S35325; MUID:93223707; PMID:8467811
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    fruit fly (Drosophila melanogaster)

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A,Residues: 1-196,'R',198-394,'D',396-512,'D',514 <RU2>
A,Cross-references: UNIPARC:UPI000016BD6A; EMBL:X70862; NID:g11143; PIDN:CAA50212.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N; Contains: protein kinage (EC 2.7.1.37)
C; Species: Drosophila melanogaster
C; Date: 19-Jul-1996 #sequence revision 01-Nov-1996 #text change 05-Oct-2004
C; Accession: 833517; 833526; 835329; A44331; 811675; 810931; 835421; 835422; 835424
B; Ruel, L.; Pantesco, V.; Lutz, Y.; Simpson, P.; Bourouis, M.
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                                                                                                                                                                                                                      YSSGEKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLAYIHSFG 186
                                                                                                                                                                                                                                                                                         KAHPWTKVFRPRTPPEAIALCSRLLEYTPTARLTPLEACAHSFFDELRDPNVKHPNGRDT 366
                              180 YSSGEKKDELYINLVLEYVPETVYRVARHPTKAKLIIPIIYVKVYMYQLFRSLAYIHSQG
                                                                                                                                                                                             SIDVWSAGCVLAELLLGQPIPPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQI
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A;Residues: 1-445, R., 447-510, DVTDS' <SIE>
A;Cross-references: UNIPARC:UD1000017A460
R;Bourouis, M.; Moore, P.; Ruel, L.; Grau, Y.; Heitzler, P.; Simpson,
EMBO J. 9, 2877-2884, 1990
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A,Status: preliminary; nucleic acid sequence not shown; not
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                                                                                                                                                                                                                                                                                                                                                                                            PALFNFTTQELSSNPPLATILIPPHAR 393
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: An early embryonic product of the A;Reference number: S11675; MUID:90361000; A;Accession: S11675
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A; Residues: 1-575 <RUE>
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A,Cross-references: UNIPROT:Q91627; UNIPARC:UPI00000FBE97; EMBL:U31862; NID:g1000734; ICSUperfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; phosphorransferase C;Keywords: ATP; phosphorransferase 75-315/Domain: protein kinase homology <KIN> F;62-315/Domain: protein kinase ATP-binding motif F;85/Active site: Lys #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLPRSLAYIHSFGICHR 190
                                                                                                                                                                                                                                                                                                                1 MSGRPRITSFAESCKPVQQPSSFGSMKVSRDKDGSKVTTVVATPGQGPDRQQEVSYTDTK 60
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                                                                                                                                                                        Length 420;
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                                                                                                                                                                                                                      9; Indels
                                                                                                                                                                   92.4%; Score 1923; DB 2;
95.0%; Pred. No. 1.6e-84;
iive 10; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NFTTQELSSNPPLATILIPPHAR 393
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nes 312; Conservative
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                                                                                                                                                                                             Local Similarity
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Best Local S:
Matches 364
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R;Ruel, L.; Panteseco, V.; Lutz, Y.; Simpson, P.; Bourouis, M.
EMBO J. 12, 1657-1669, 1993
A;Title: Functional significance of a family of protein kinases encoded at the shaggy loc A;Title: Functional significance of a family of protein kinases encoded at the shaggy loc A;Reference number: S35325; MUD:93223707; PMID:8467811
A;Recession: S35323
A;Retus: preliminary
A;Molecule Cype: mRNA
A;Residues: 1-1067 <RUE>
A;Cross-references: UNIPARC:UPI000013591B; EMBL:X70864; NID:g11147; PIDN:CAA50214.1; PID
A;Genetics:
A;Genetics:
A;Genetics:
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                                                       403
                                                                                                     404 HSLGICHRDIKPONLLLDPETAVLKLCDFGSAKQLLHGEPNVSYICSRYKRAPELIFGAI 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYTSSIDVWSAGCVLABLLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFK 302
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                                                                                                                                             DYTSSIDVWSAGCVLABLLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFK 302
                                                                                                                                                                                                      FPOIKAHPWTKVFRPRTPPEAIALCSRLLEYTPTARLTPLEACAHSFFDELR-DPNVKHP 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FPQIKAHPWIKVFRPRTPPEAIALCSRLLEYTPTARLTPLEACAHSFFDELR-DPNVKHP 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                             664 LYFFYSSGEKRDEVFLNLVLEYIPETVYKVARQYAKTKQTIPINFIRLYMYQLFRSLAYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 LYFFYSSGEKRDEVFLNLVLEXIPETVYKVARQYAKTKQTIPINFIRLYMYQLFRSLAYI
                                                                                    183 HSFGICHRDIKPQNLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGAT
                                                                                                                                                                                                                      7 EGGGMSGRPRITSFAESC----KPVQQPSAFGSMKVSRDKDGSKVTTVVATPGQGPDRPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSPGICHRDIKPQNLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGAT
                                                                                                                                                                                                                                                                                                                                                                  protein kinase sgg46 (BC 2.7.1.-) - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Length 1067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.1%; Score 1542.5; DB 75.9%; Pred. No. 3.5e-66; ive 36; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: FlyBase:FBgn0003371
Ckeywords: ATP; phosphotransferase
F;605-66(Domain: protein kinase homology <KIN>F;613-621/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                             613
                                                                                                                                                                                                                                                               NGRDTPALFNFTTQELSSNPPLATILIPPH 391
                                                                                                                                                                                                                                                                                  Best Local Similarity 75.9%
Matches 296; Conservative
                                                                                                                                               243
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                                                                                                                                                                                                                                                                                              VWSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQIKAH 309
                                                                                                                                                                                                                                                                                                                                                                                                                   VWSAGCVLAELLLGQPIFPGDSGVDQLVEVIKVLGTPTREQIREMNPNYTEFKFPQIKSH 297
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                                         phosphotransferase;
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                                                                                                                                                             11 MSGRPRITSFAESCKPVQQPS-AFGSMKVSRDKDGSKVTTVVATPGQGPDRPQEVSYTDT
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                                                                                                     575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 74.1%; Score 1542.5; DB 2; Length Local Similarity 75.9%; Pred. No. 2.5e-66; hes 296; Conservative 36; Mismatches 47; Indels
                                                                                                     Length
                                                                                                                               41; Indels
            A Gene: FlyBase: sgg
A,Cross-references: FlyBase: FBgn0003371
CJKeywords alterative splicing; ATP; phosphoprotein;
F,52-313/Domain: protein kinase homology «KIN»
F,50-68/Region: protein kinase ATP-binding motif
                                                                                                     DB 2;
                                                                                                    Score 1590.5; DB 2
Pred. No. 1.1e-68;
                                                                                          76.4%; Scott 79.6%; Pred. No. 1.1.
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                                                                                                                  Best Local Similarity 79.69
Matches 305; Conservative
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R; Takvorian, A.; Schwebel-Dugue, N.; Dornelas, M.C.; Tichtindky, G.; Twell, D.; Kreis, M submitted to the EMBL Data Library, October 1996
A; Reference number: 214970
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A,Experimental source: cultivar Samsun NN; tissue-type pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TREQIREMNPNYTEFKFPQIKAHPWTKVFRPRTPPEAIALCSRLLEYTPTARLTPLEACA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YVKLYMYQLFRSLAYIHSFGICHRDIKPQNLLLDPDTAVLKLCDFGSAKQLVRGEPNVSY 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 MRKLDHCNIVRLRYFFYSSGEKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKL 170
                                                                                                                                                                                                                                                                                                                                                   47 VTTVVATPGQGPDRPQEVSYTDTKVIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 ELQIMRKLDHCNIVRLRYFFYSSGEKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVI 166
                                                                                                                                                                                                                                                                                  6 MPSAG----GKHRTDAMLVD----KLPEEINEMKIRDDKAEKEMEAAVVDGNGTEKGHII 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              shaggy protein kinase (EC 2.7.1.-) 6 - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; phosphotransferase; protein kinase P;140-401/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 ICSRYYRAPELIFGATDYTSSIDVWSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSFFDELRDPNVKHPNGRDTPALFNFTTQEL-SSNPPLATILIPPHAR 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 409;
                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                 4 MPMEGGGMSGRPRITSFAESCKPVQQPSAFGSMKVSRDK
                                                                                                           Query Match 62.3%; Score 1296; DB 2; Best Local Similarity 62.3%; Pred. No. 7.1e-55; Matches 254; Conservative 49; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.3%; Score 1275.5; DB ; ilarity 61.7%; Pred. No. 7.4e-54; Conservative 49; Mismater.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: T03601
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                        F;80-88/Region: protein kinase ATP-binding motif F;103/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 MSGRPRITSFAESCKPVQQPSAFGSMKVSRDK---
F;72-332/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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Best Local Simi
Matches 250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNIPARC: UPI000007BD45; EMBL: AL034393; PIDN: CAA22311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QTLPVIYVKLYMYQLFRSLAYIHSFGICHRDIKPQNLLLDPDTAVLKLCDFGSAKQLVRG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPNVSYICSRYYRAPELIFGATDYTSSIDVWSAGCVLAELLLGQPIFPGDSGVDQLVEII 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVLGTPTREQIREMNPNYTEFKFPQIKAHPWTKVFRPRTPPEAIALCSRLLEYTPTARLT 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRPKNRELQIMRKLDHCNIVRLRYFFYSSGEKKDEVYLNLVLDYVPETVYRVARHYSRAK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSGKOVTMVVASVATDGVDQQVEISYYDQKVIGNGSFGVVFLAKLSTTNEMVAIKKVLQD 70
                                                                                                                                                                                               hypothetical protein Y18D10A.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T2620
B;Harris, B.
Submitted to the EMBL Data Library, December 1998
A;Reference number: Z20226
A;Accession: T26520
A;Accession: T26520
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: CESP:Y18D10A.5
A;Gene: CESP:Y18D10A.5
A;Introns: 31/3; 121/2; 313/3
C;Superfamily: kinase-related transforming protein; protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: PSK4
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphoprotein; phosphotransferase; protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 64.5%; Score 1342.5; DB 2; Length al Similarity 77.2%; Pred. No. 4e-57; 254; Conservative 33; Mismatches 41; Indels
                                 NGRDTPALFNFTTQELSSNPPLATILIPPH 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341 PLEACAHSFFDELRDPNVKHPNGRDTPAL 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: clone Y18D10A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-362 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 254
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362
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                                                                                                                                                                                                                                                                                     C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48637
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, submitted to the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 VVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSGEKKDEVYL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLAYIH-SFGICHRDIKPQNL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 AELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQIKAHPWTKVFRP 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 5
A;Introns: 39/3; 70/3; 90/3; 181/3; 206/3; 225/3; 272/3; 289/3; 321/3; 349/
A;Note: T15N1.130
C;Superfamily: kinase-related transforming protein; protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 PEGINEMKIKDDKEMEAAVVDGNGTETGHIIVTTIGGKNGQPKQTISYMAERIVGGSFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 NLVLEYVPETVYRVSKHYSRANQRMPIIYVKLYTYQICRALAYIHGGVGVCHRDIKPQNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 PSAFGSMKVSRDK-----DGSKVTT----VVATPGQGPDRP-QEVSYTDTKVIGNGSFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLDPDTAVLKLCDPGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDVWSAGCVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q8VZD5; UNIPARC:UPI00000A9FA8; EMBL:AL163792 A;Experimental source: cultivar Columbia; BAC clone T15N1 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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RjGeisel, C.
Rideisel, C.
Ajbenitted to the EMBL Data Library, April 1998
Ajbeciption: The sequence of A. thaliana F6N23.
Ajbeciption: Tolass
Ajbe
                                                                                                                                                                                                                       protein kinase MSK-3-like - Arabidopsis thaliana
                                                                                                                                                                                                                                                          N;Alternate names: protein T15N1.130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Reference number: 224493
A, Accession: T48637
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-408 < BEV>
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PEHMR 470
                                  466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             shaggy protein kinase (EC 2.7.1.-) 91 [similarity] - common tobacco C; Species: Nicotiana tabacum (common tobacco) C; Species: Nicotiana tabacum (common tobacco) C; Species: Nicotiana tabacum (common tobacco) C; Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004 C; Accession: T02297
R; Tichtinsky, G; Tavares, R; Takvorian, A; Schwebel-Dugue, N; Twell, D; Kreis, M. Biochim: Biophys. Acta 1442, 261-273, 1998
A; Title: An evolutionary conserved group of plant GSK-3/shaggy like protein kinase genes A; Reference number: 214641; MulD:99023747; PMID:9804971
A; Reference number: 214641; MulD:99023747; PMID:9804971
A; Residues: 1-71 < TIC>
A; Accession: T02297
A; Residues: 1-71 < TIC>
A; Residues: 1-71 < TIC>
A; C; Superimental source: cultivar Samsun NN; tissue-type pollen C; Genetics: NSK 91
C; Superimental source: cultivar Samsun NN; tissue-type pollen C; Superimental source: pollen C; Superimental source: cultivar Samsun NN; tissue-type pollen C; Superimental Samsun Nn; tissue-type
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                                                                                                                                                                                                                                                                                                                                                                                                     EIRCMNPNYTEPKFPQIKAHPWHKIFHKRMPPEAVDLVSRLLQYSPILRCTALEACAHPF 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 LVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSGEKKDEVYLNLVLDYVPETVY 150
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Best Local Similarity 60.55
Matches 257; Conservative
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120 MRLLDHPNVVSLKHCFFSTTB-KDELYLNLVLEYVPETVSRVIRHYNKMNQRMPMIXVKL 178
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             52 ATPGQGPDRP-QEVSYTDTKVIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQI 110
                                                MRKLDHCN1VRLRYFFYSSGEKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPV1YVKL
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Job time : 42 secs
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S17642
protein kinase MSK-3 (EC 2.7.1.-) [similarity] - alfalfa
C.Species: Medicago sativa (alfalfa)
C.Species: May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C.Accession: 337642
A.Title: The MsK family of alfalfa protein kinase genes encodes homologues of shaggy/gly
A.Reference number: S37642; MUID:94004996; PMID:8401615
A.Accession: S37642
A.Molecule type: mRNA
A.Residues: I-412 < PAPA
A.Residues: I-412 < PAPA
A.Residues: I-412 < PAPA
A.Residues: The Phosphotransforming protein; protein kinase homology
C.Superfamily: kinase-related transforming protein; protein kinase homology < KIN>
F.31-334 Domain: protein kinase ATP-binding motif
F:104/Active site: Lys #status predicted
A;Residues: 1-472 cGEI>
A;Cross-references: UNIPROT:Q96287; UNIPARC:UPI000000056A; EMBL:AF058919; NID:g3047100;
C;Genetics:
C;Genetics:
A;Gene: ATSP:F6N23.11
A;Map position: 5
A;Introns: 21/3; 134/3; 154/3; 245/3; 270/3; 289/3; 336/3; 353/3; 385/3; 413/3; 4;Introns: 21/3; 103/3; 134/3; 154/3; 245/3; 270/3; 289/3; 336/3; 353/3; 385/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 413/3; 41
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                                                                                                                                                                                                                                                                                                                                                                                                        60.5%; Score 1258; DB 1; Length 472; 61.6%; Pred. No. 5e-53; ive 54; Mismatches 74; Indels 2
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Matches 250; Conservative 5
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